

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:11 ; Search time 15.53 seconds
(without alignments)
1283.098 Million cell updates/sec

Title: US-09-405-940-1
Perfect score: 1664
Sequence: 1 MGTRLLCWAALCLLGADHTG.....AVLVSAVLMMVKKRDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1094.5	65.8	307	2 S03716	T-cell receptor be
2	1048.5	63.0	309	2 S18894	T-cell receptor be
3	1036	62.3	306	2 S25118	T-cell receptor be
4	944	56.7	179	2 C25777	T-cell receptor be
5	907	54.5	177	1 RWUUCY	T-cell receptor be
6	856.5	51.5	267	2 P0064	T-cell receptor be
7	772.5	46.4	178	2 P0075	T-cell receptor be
8	770	46.3	177	2 B49054	T-cell receptor be
9	763.5	45.9	178	2 P0076	T-cell receptor be
10	750	45.1	177	1 RWVTC	T-cell receptor be
11	741	44.5	173	2 A46547	T-cell receptor be
12	741	44.5	319	1 RWBBB	T-cell receptor be
13	736	44.2	173	1 RWSLC	T-cell receptor be
14	732.5	44.0	174	2 A49828	T-cell receptor be
15	731	43.9	173	1 RWSBC	T-cell receptor be
16	724	43.5	173	2 B46547	T-cell receptor be
17	724	43.5	237	2 A30602	T-cell receptor be
18	710	42.7	173	2 G27579	T-cell receptor be
19	661	39.7	141	2 S03495	T-cell receptor be
20	653	38.2	139	2 S38393	T-cell receptor be
21	632.5	38.0	135	2 S57882	T-cell receptor PS
22	621	37.3	151	2 S24064	T-cell receptor be
23	570	34.3	114	2 PT0733	T-cell receptor be
24	570	34.3	115	2 S22035	T-cell receptor be
25	526.5	31.6	125	2 B45806	T-cell receptor be
26	526	31.6	269	2 I46884	T-cell receptor be
27	510.5	30.7	129	2 S7884	T-cell receptor WI
28	476	28.6	114	2 PT0734	T-cell receptor be
29	476	28.6	115	2 S22038	T-cell receptor be

30	471.5	28.3	134	2 B24747	T-cell receptor be
31	468.5	28.2	135	2 S38366	T-cell receptor be
32	463	27.8	113	2 S22039	T-cell receptor be
33	454	27.3	132	2 S30441	T-cell receptor be
34	447	26.9	115	2 S22036	T-cell receptor be
35	435	26.1	114	2 G32537	T-cell receptor be
36	433	26.0	133	1 RWU7B	T-cell receptor be
37	431	25.9	115	2 S22037	T-cell receptor be
38	421	25.3	114	2 S17388	T-cell receptor be
39	417.5	25.1	148	2 S36133	T-cell receptor be
40	408	24.5	101	2 I32537	T-cell receptor be
41	407.5	24.5	133	2 S57880	T-cell receptor HW
42	398	23.9	114	2 S17387	T-cell receptor be
43	391	23.5	145	2 S21651	T-cell receptor be
44	389.5	23.4	140	2 S36942	T-cell receptor be
45	389.5	22.2	102	2 S03492	T-cell receptor be

ALIGNMENTS

RESULT 1

S03716
T-cell receptor beta chain precursor (F5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 05-Nov-1999
C:Accession: S03716
R:Palmer, M.S.; Bentley, A.; Gould, K.; Townsend, A.R.M.
Nucleic Acids Res. 17, 2353, 1989
A:Title: The T cell receptor from an influenza-A specific murine CTL clone.
A:Reference number: S03715; MUID:99202046
A:Accession: S03716
A:Molecule type: mRNA
A:Residues: 1-307 <PAL>
A:Cross-references: EMBL:X14388; NID:g54668; PIDN:CAA32563.1; PID:g54669
C:Keywords: T-cell receptor
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-307/Product: T-cell receptor beta chain #status predicted <MAT>

Query Match		65.8%	Score 1094.5;	DB 2;	Length 307;
Best Local Similarity		68.6%	Pred. No. 7.6e-78;		
Matches 214;		Conservative 34;	Mismatches 59;	Indels 5;	Gaps 2;
Qy	1	MGTRLLCWAALCLLGADHTGAGVSQTPSNKYTERGKDVELECDPISGHTALYWRQSLGQ	60		
Db	1	MAPRLFLCLVCLFRAEPTNAGVQTIPRHKVTGKQEATLWCEPISGHSVAVFWYRQITVQ	60		
Qy	61	GPEFLIYFGGTGAADDGSLPNDREFAVEPEGSVSTLKTORTQGDGSAAYLRAGVAGWSS	120		
Db	61	GLEFLIYFRNAPIDDDSGMPKRFSAQPNOSHSTLKIQTQDQSAVYLCS-SSRTGG	119		
Qy	121	YNEQYFGTGLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFPDPHVELSW	180		
Db	120	HAEOFFGFGTGLTVLEDLRNVTTPKVSLEFEPKAEIANKQKATLVCLARGFPDPHVELSW	179		
Qy	181	WVNGKEVHSGVSTDPQPKQEPALNDSRYCLSSRLRSVATFWQPNRHFRCQVFGYGLSE	240		
Db	180	WVNGKEVHSGVSTDPQAYKE---SNVSYCLSSRLRSVATFWHPRNHFRCQVFGHGLSE	235		
Qy	241	NDEMTQDRAKPVQTVSAEAWGRADCGFTSEYQOQGLVSATILYEILIGKATLVAVLSA	300		
Db	236	EDKWPESGPKPVTQNISAEAWGRADCGITSASYHQGLVSATILYEILIGKATLVAVLSG	295		
Qy	301	LVLMMVKKDS	312		
Db	296	LVLMMVKKNS	307		

RESULT 2

S18894
T-cell receptor beta chain precursor - human
C:Species: Homo sapiens (man)

5

2.

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RESULT      5
RWZUCY
T-cell receptor beta-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 02-Sep-1997
C:Accession: B25777; A02133
R:Tunnacliffe, A.; Keifford, R.; Milstein, C.; Forster, A.; Rabbitts, T.H.
Proc. Natl. Acad. Sci. U.S.A. 82: 5068-5072, 1985

```

[illegible]

A;Reference number: A94052; MUID:85242712

A;Accession: A94052

A;Molecule type: mRNA

A;Residues: 1-319 <ANG>

R;Wage: R

Submitted to the Protein Sequence Database, April 1987

A;Reference number: A94616

A;Contents: corrections to residues 79-83 and 104-105

A;Accession: A94616

A;Molecule type: mRNA

A;Residues: 79-83,104-105 <MAG>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: glycoprotein; heterotetramer; T-cell receptor; transmembrane protein

F;166-240/Domain: immunoglobulin homology <IMM>

F;292-313/Domain: transmembrane #status predicted <TM>

F;314-318/Domain: intracellular #status predicted <INT>

F;147,164,254,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.5%; Score 741; DB 1; Length 319;

Best Local Similarity 76.5%; Pred. No. 2.3e-50;

Matches 140; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 130 TRUTVLELDKNVPEVAFPESEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHS 189

Db 137 TPHFPEDLANVAPQVVPDPSEAEINKTKATLVCLAKDFPDHVELSWVNGKEVHN 196

QY 190 GVSTDPQPLKEQPALNDSRYCLSSRLRVSAFWQNPNRNHFRCQVQYGLSENDEWTDRA 249

Db 197 GVSTDPQPYKQDPKSDHSKYLCLSSRLRVSAFAFWNPNRNFRCQVQFGLTDDDEWTYNS 256

QY 250 KPVTVISAEAWGRADCGFTSESQOQVLSATILYELLGKATLVAVLSALVLMAMVKR 309

Db 257 KPTQNTSATRGRADCGISSAYQOQVLSATVYELLGKATLVAVLSALVLMAMVKR 316

QY 310 KDS 312

Db 317 KDS 319

RESULT 13

RWMSLC

T-cell receptor beta-1 chain C region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 16-Aug-1996

C;Accession: B93336; A93325; A23572; A02135

R;Gascoigne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalier, J.; Davis, M.M.

Nature 310, 387-391, 1984

A;Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and

A;Reference number: A93336; MUID:84270704

A;Accession: B93336

A;Molecule type: DNA

A;Residues: 1-173 <GAS>

A;Cross-references: GB:M26053

A;Experimental source: strain B10.A, cytotoxic T lymphocyte

R;Hedrick, S.M.; Nielsen, E.A.; Kavalier, J.; Cohen, D.I.; Davis, M.M.

Nature 308, 153-158, 1984

A;Title: Sequence relationships between T-cell receptor polypeptides and immunoglobulin

A;Reference number: A93325; MUID:84142271

A;Accession: A93325

A;Molecule type: mRNA

A;Residues: 1-69, 'H', 71-173 <HED>

A;Cross-references: GB:K01080

A;Experimental source: clone 86T1

R;Morinaga, T.; Fotedar, A.; Singh, B.; Wegmann, T.G.; Tamaoki, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 8163-8167, 1985

A;Title: Isolation of cDNA clones encoding a T-cell receptor beta-chain from a beef insu

A;Reference number: A94078; MUID:86068062

A;Accession: A23572

A;Molecule type: mRNA

A;Residues: 1-173 <MOR>

A;Cross-references: GB:M11456

A;Note: the authors translated the codon TAT for residue 134 as Val

C;Genetics:

A;Introns: 1/1; 126/1; 132/1; 163/3

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: glycoprotein; heterotetramer; receptor; T-cell; transmembrane protein

F;24-94/Domain: immunoglobulin homology <IMM>

F;152-168/Domain: transmembrane #status predicted <TM>

F;169-173/Domain: intracellular #status predicted <INT>

F;31-71/Disulfide bonds: #status predicted

F;67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.2%; Score 736; DB 1; Length 173;

Best Local Similarity 79.1%; Pred. No. 2.6e-50;

Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

QY 136 EDLKNVPEVAFPESEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHSGVSTDP 195

Db 1 EDLRNVTTPKVSIFPEPSKAEIAKOKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDP 60

QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQNPNRNHFRCQVQYGLSENDEWTDQRAKPVTVQI 255

Db 61 QAYKE-----SNYSYCLSSRLRVSAFWNPNRNFRCQVQFHGLSEDKWPEGSPKPVTON 116

QY 256 VSAEAWGRADCGFTSESQOQVLSATILYELLGKATLVAVLSALVLMAMVKRDS 312

Db 117 ISAEAWGRADCGITTSASYOQVLSATILYELLGKATLVAVLSTLVVMAMVKRNS 173

RESULT 14

A49828

T-cell receptor beta chain C region (Cbeta1) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: A49828

R;Blankenhorn, E.P.; Stranford, S.A.; Smith, P.D.; Hickey, W.F.

Eur. J. Immunol. 21, 2033-2041, 1991

A;Title: Genetic differences in the T cell receptor alleles of LEW rats and their enc

A;Reference number: A49828; MUID:91364772

A;Accession: A49828

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-174 <BLA>

A;Cross-references: GB:S60762; NID:g235079; PIDN:AAB19719.1; PID:g235080

A;Experimental source: Lewis

A;Note: sequence inconsistent with nucleotide translation

A;Note: sequence extracted from NCBI backbone (NCBIN:60762, NCBI:60764)

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: T-cell receptor

F;24-95/Domain: immunoglobulin homology <IMM>

Query Match 44.0%; Score 732.5; DB 2; Length 174;

Best Local Similarity 78.0%; Pred. No. 4.9e-50;

Matches 138; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

QY 136 EDLKNVPEVAFPESEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHSGVSTDP 195

Db 1 EDLKTVPKVSIFPESEAEIAKOKATLVCLARGFFPDHVELSWVNGKEIRNGVSTDP 60

QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQNPNRNHFRCQVQYGLSENDEWTDQRAKPVTVQI 255

Db 61 QATKES---NNITYCLSSRLRVSAFWNPNRNFRCQVQYGLTEEDNWSDESPKPVTON 117

QY 256 VSAEAWGRADCGFTSESQOQVLSATILYELLGKATLVAVLSALVLMAMVKRDS 312

Db 118 ISAEAWGRADCGITTSASYOQVLSATILYELLGKATLVAVLSTLVVMAMVKRKS 174

RESULT 15

RWMSBC

T-cell receptor beta-2 chain C region - mouse

C;Species: Mus musculus (house mouse)

C:Date: 03-Aug-1984 #sequence_revision 28-Feb-1986 #text_change 05-Sep-1997
C:Accession: A93336; B93333; A02134
R:Gascoigne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalier, J.; Davis, M.M.
Nature 310, 387-391, 1984
A:Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and J
A:Reference number: A93336; MUID:84270704
A:Accession: A93336
A:Molecule type: DNA
A:Residues: 1-173 <GAS>
A:Experimental source: strain B10.A, cytotoxic T lymphocyte
R:Saito, H.; Kranz, D.M.; Takagaki, Y.; Hayday, A.C.; Eisen, H.N.; Tonegawa, S.
Nature 309, 757-762, 1984
A:Title: Complete primary structure of a heterodimeric T-cell receptor deduced from cDNA
A:Reference number: A93333; MUID:84245824
A:Accession: B93333
A:Molecule type: mRNA
A:Residues: 1-49, 'R', 51-69, 'H', 71-173 <SAI>
A:Experimental source: BALB.B, clone 2C, cytotoxic T lymphocyte
C:Genetics:
A:Introns: 1/1; 126/1; 132/1; 163/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; receptor; T-cell; transmembrane protein
F:24-94/Domain: immunoglobulin homology <IMM>
F:147-168/Domain: transmembrane #status predicted <TM>
F:169-173/Domain: intracellular #status predicted <INT>
F:67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.9%; Score 731; DB 1; Length 173;
Best Local Similarity 78.5%; Pred. No. 6.4e-50;
Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;

QY 136 EDLKNVPEPEVAVPEPSEAEITSHQKATLVCLATGYPDPHVELSWVNGKEVHSGVSTDP 195
Db 1 EDLRNVTTPPKVSLPEPSKAEIANKQKATLVCLARGFPDPHVELSWVNGKEVHSGVSTDP 60
QY 196 QPLKEQPALNDSRYCLSSRLRVSATFWQNPDRNHFRCQVQFGLSENDEWTDRAKPVTOI 255
Db 61 QAYKE---SNYSYCLSSRLRVSATFWHNPDRNHFRCQVQFGLSEEDKNWPEGSPKPVTON 116
QY 256 VSAZAWGRADCGFTSEYQOGVLSATILYEILGKATLYAVLVSAVLMAMVKKDS 312
Db 117 ISAEAWGRADCGTTSASYHQVLSATILYEILGKATLYAVLVSAVLMAMVKKNS 173

Search completed: October 11, 2000, 06:09:02
Job time: 51 sec

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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:11 ; Search time 9.53 Seconds
(without alignments)
1021.047 Million cell updates/sec

Title: US-09-405-940-1

Perfect score: 1664
Sequence: 1 MGTRLLCWAALCLLGADHTG.....AVLVSAVLMAVVKRKDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1037	62.3	321	1	TCB_FIV	P11364 feline leuk
2	907	54.5	177	1	TCB_HUMAN	P01850 homo sapien
3	741	44.5	319	1	TCB1_RABIT	P06333 oryctolagus
4	736	44.4	173	1	TCB1_MOUSE	P01852 mus musculu
5	731	43.9	173	1	TCB2_MOUSE	P01851 mus musculu
6	433	26.0	133	1	TVB2_HUMAN	P04435 homo sapien
7	367.5	22.1	134	1	TVB7_MOUSE	P06320 mus musculu
8	337	20.3	135	1	TVB1_HUMAN	P01733 homo sapien
9	249.5	15.0	135	1	TVB1_MOUSE	P01734 mus musculu
10	183	11.0	122	1	TVB5_MOUSE	P04213 mus musculu
11	180.5	10.8	136	1	TVB4_MOUSE	P04212 mus musculu
12	170	10.2	104	1	LAC2_RAT	P20767 rattus norv
13	165	9.9	133	1	TVB2_MOUSE	P01735 mus musculu
14	161.5	9.7	130	1	TVB8_MOUSE	P06321 mus musculu
15	160.5	9.6	213	1	II41_HUMAN	P15814 homo sapien
16	154	9.3	105	1	LAC1_MOUSE	P01843 mus musculu
17	152.5	9.2	105	1	LAC_PIG	P01846 sus scrofa
18	152	9.1	103	1	LAC_CHICK	P20763 gallus gall
19	150	9.0	106	1	KACB_RABIT	P01839 oryctolagus
20	149.5	9.0	391	1	MUCB_HUMAN	P04220 homo sapien
21	149	9.0	104	1	LAC3_MOUSE	P01845 mus musculu
22	147.5	8.9	104	1	LAC1_RAT	P20766 rattus norv
23	146.5	8.8	105	1	LAC_RABIT	P01847 oryctolagus
24	146	8.8	454	1	MUC_HUMAN	P01871 homo sapien
25	144	8.7	458	1	MUC_RABIT	P03988 oryctolagus
26	144	8.7	479	1	MUCM_RABIT	P04221 oryctolagus
27	143	8.6	299	1	ALC_RABIT	P01879 oryctolagus
28	142	8.5	104	1	LAC2_MOUSE	P01844 mus musculu
29	142	8.5	111	1	LV3B_HUMAN	P07048 homo sapien
30	140.5	8.4	104	1	KAC6_RABIT	P03984 oryctolagus
31	140.5	8.4	120	1	TVB3_MOUSE	P01736 mus musculu
32	140	8.4	344	1	ALC_MOUSE	P01878 mus musculu
33	139.5	8.4	105	1	LAC_HUMAN	P01842 homo sapien

34	137.5	8.3	438	1	HVC2_HETFR
35	137	8.2	368	1	HA14_MOUSE
36	136.5	8.2	421	1	EPC_MOUSE
37	135.5	8.1	353	1	ALC1_HUMAN
38	135.5	8.0	353	1	ALC1_GORGO
39	133	8.0	340	1	ALC2_HUMAN
40	132.5	8.0	399	1	GCAM_MOUSE
41	132	7.9	135	1	TVCL_MOUSE
42	131.5	7.9	298	1	HA19_MOUSE
43	131.5	7.9	365	1	HA12_MOUSE
44	131.5	7.9	393	1	HVC3_HETFR
45	131	7.9	136	1	TVC_HUMAN

ALIGNMENTS

```

RESULT 1
TCB_FLV
ID TCB_FLV STANDARD; PRT; 321 AA.
AC P11364;
DT 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DE T-CELL RECEPTOR BETA CHAIN T17T-22 PRECURSOR.
GN V-TCR.
OS Feline leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses.
RN [1]
RX MEDLINE; 87144638.
RA Fulton R., Forrest D., McFarlane R., Onions D., Neil J.C.;
RT "Retroviral transduction of T-cell antigen receptor beta-chain and
RL myc genes.";
RN Nature 326:190-194(1987).
[2]
RN REVISION TO 158-159.
RA Fulton R.;
RL Submitted (DEC-1987) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05155; CAA38801.1;
DR PIR; C26600; RRMVTC.
DR PIR; B26600; RRMVTV.
DR PFAM; PF00047; ig; 2.
KW T-cell; Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 28
FT CHAIN 29 321 T-CELL RECEPTOR BETA CHAIN T17T-22.
FT DOMAIN 29 122 V SEGMENT.
FT DOMAIN 123 128 D SEGMENT.
FT DOMAIN 129 144 J SEGMENT.
FT DOMAIN 145 321 C REGION.
SQ SEQUENCE 321 AA; 355581 MW; 11D2C3BF56811129 CRC64;

```

	Query Match	62.3%	Score 1037	DB 1	Length 321
	Best Local Similarity	66.1%	Pred. No. 3.7e-60		
	Matches 207	Conservative 26	Mismatches 78	Indels 2	Gaps 2
QY	1	MGTRLLCAAALCULGADHTGAGVSTPSNKVTEKGDVEILRCDPISGHTALYVYRSLGQ	60		
DB	10	MGRLLCCVALLCULGAPDAGTGLTPRHLYKARGQQVTLSCFPISGHLSLVYQQAVGQ	69		
QY	61	GPFLIYFQGTGAADSLGPNDRFFAVRPGSVSTLKIQRTEQGDSSAAYLRAGVAAQWSS	120		
DB	70	GPOLLTYNREERKGNFP-ERFSAQFPDHSHELANTSLKLTDSALYLCASSPNEDSE	128		

QY 121 YNEQ-YFGPGRTRVLVLEDKNVPPEVAVFEPSEAEISHTQKATLVCLATGYPDPHVELS 179
 DB 129 YGETLYFGESRLTVVYEDLKKVSPKVTVPFSEAEISRTLKATLVCLATGYPDPHVELS 188
 QY 180 WYNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFTWQPNRHFRCQVQFYGLS 239
 DB 189 WYNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAFTWQPNRHFRCQVQFYGLS 248
 QY 240 ENDEWTDRAKPVTVQTSYAEAGNADCGFTSESYQQGVLSATILYEILLGKATLVAVLSV 299
 DB 249 KDWQDYPEAKPVTVQTSYADTWGRADCGFTSASYQQGVLSATILYEILLGKATLVAVLSV 308
 QY 300 ALVLMAMVKKRDS 312
 DB 309 VLALMAKVRKDS 321

RESULT 2

TCB1_HUMAN STANDARD; PRT; 177 AA.
 AC P01850;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE T-CELL RECEPTOR BETA CHAIN C REGION.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP MEDLINE; 84142269.
 RA Yanagi Y., Yoshikai Y., Leggett K., Clark S.P., Aleksander I.,
 RA Mak T.W.;
 RT "A human T cell-specific cDNA clone encodes a protein having
 RT extensive homology to immunoglobulin chains.";
 RL Nature 308:145-149(1984).
 DR PIR; A02133; RWHUCY.
 DR PFAM; PF00047; ig: 1.
 KW T-cell; Receptor.
 FT NON_TER 1
 SQ SEQUENCE 177 AA; 19898 MW; 9242AFAA3E3DB4AE CRC64;

Query Match 54.5%; Score 907; DB 1; Length 177;
 Best Local Similarity 97.7%; Pred. No. 1.5e-69;
 Matches 172; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 136 EDLKNVPPEVAVFEPSEAEISHTQKATLVCLATGYPDPHVELSWWNGKEVHSGVSTDP 195
 DB 1 EDLKNVPPEVAVFEPSEAEISHTQKATLVCLATGYPDPHVELSWWNGKEVHSGVSTDP 60
 QY 196 QPLKEQPALNDSRYCLSSRLRVSAFTWQPNRHFRCQVQFYGLSENDEWTDRAKPVTVQI 255
 DB 61 QPLKEQPALNDSRYCLSSRLRVSAFTWQPNRHFRCQVQFYGLSENDEWTDRAKPVTVQI 120
 QY 256 VSAEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKKRD 311
 DB 121 VSAEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKKRD 176

RESULT 3

TCB1_RABIT STANDARD; PRT; 319 AA.
 AC P06333;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE T-CELL RECEPTOR BETA CHAIN ANA 11.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 85242712.
 RA Angiolillo A.L., Lamoyi E., Bernstein K.E., Mage R.G.;
 RT "Identification of genes for the constant region of rabbit T-cell
 RT receptor beta chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4498-4502(1985).
 RN [2]
 RP REVISIONS TO 79-83 AND 104-105.
 RA Mage R.G.;
 RL Submitted (APR-1987) to the PIR data bank.
 DR PIR; A02136; RWRBB.
 DR PFAM; PF00047; ig: 1.
 KW T-cell; Receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 142 273 C REGION.
 FT TRANSMEM 292 313
 FT DOMAIN 314 319 CYTOPLASMIC TAIL.
 FT CARBOHYD 147 147 POTENTIAL.
 FT CARBOHYD 164 164 POTENTIAL.
 FT CARBOHYD 254 254 POTENTIAL.
 FT CARBOHYD 262 262 POTENTIAL.
 SQ SEQUENCE 319 AA; 36068 MW; AAD2C3035ED45306 CRC64;

Query Match 44.5%; Score 741; DB 1; Length 319;
 Best Local Similarity 76.5%; Pred. No. 2.9e-55;
 Matches 140; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 130 TRLVLEDKNVPPEVAVFEPSEAEISHTQKATLVCLATGYPDPHVELSWWNGKEVHS 189
 DB 137 TPLHFPEDLANVSAPQVYVDFPSEAEINKTKATLVCLAKDFYDPHVELSWWNGKEVHN 196
 QY 190 GVSTDPQLKEQPALNDSRYCLSSRLRVSAFTWQPNRHFRCQVQFYGLSENDEWTDRA 249
 DB 197 GVSTDPQLKEQPALNDSRYCLSSRLRVSAFTWQPNRHFRCQVQFYGLSENDEWTDRA 256
 QY 250 KPVTVQTSYAEANGRADCGFTSESYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKKR 309
 DB 257 KPITQNTISATHTGRADCGISSASYQQGVLSATILYEILLGKATLVAVLSALVLMAMVKKR 316
 QY 310 KDS 312
 DB 317 KDS 319

RESULT 4

TCB1_MOUSE STANDARD; PRT; 173 AA.
 AC P01852;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE T-CELL RECEPTOR BETA-1 CHAIN C REGION.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE 86T1).
 RC STRAIN-B10.A;
 RX MEDLINE; 84270704.
 RA Gascolgne N.R.J., Chien Y., Becker D.M., Kavalier J., Cohen D.I., Davis M.M.;
 RT "Genomic organization and sequence of T-cell receptor beta-chain
 RT constant- and joining-region genes.";
 RL Nature 310:387-391(1984).
 RN [2]
 RP SEQUENCE FROM N.A. (CLONE 86T1).
 RX MEDLINE; 84142271.
 RA Hedrick S.M., Nielsen E.A., Kavalier J., Cohen D.I., Davis M.M.;
 RT "Sequence relationships between putative T-cell receptor polypeptides
 RT and immunoglobulins.";
 RL Nature 308:153-158(1984).
 CC -1- MISCELLANEOUS: REF.2 AUTHORS TRANSLATED THE CODON TAT FOR RESIDUE
 CC 134 AS VAL.
 CC -1- MISCELLANEOUS: CLONE B10.A WAS ISOLATED FROM A CYTOTOXIC T


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CC LYMPOCYTE.
CC -!- MISCELLANEOUS: CLONE 86T1 WAS ISOLATED FROM A CYTOTOXIC T
CC LYMPOCYTE.
DR PIR; A02135; RMS1C.
DR PFAM; PF00047; 1g; 1.
KW T-cell; Receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 146 C REGION.
FT TRANSMEM 146 167 POTENTIAL.
FT DOMAIN 168 173 CYTOPLASMIC TAIL.
FT VARIANT 70 70 Y -> H (IN CLONE 86T1).
FT SEQUENCE 173 AA; 19346 MW; F9B4735E46D3E4D7 CRC64;
SQ

Query Match 44.2%; Score 736; DB 1; Length 173;
Best Local Similarity 79.1%; Pred. No. 3.6e-55;
Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

QY 136 EDLKNVPPEVAVFPSEAEISHTQKATLVCLATGTFYDPDHVELSWWVNGKEVHSGVSTDP 195
DB 1 EDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDP 60
QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFGLSENDEWTDQRAKPTQI 255
DB 61 QAYKE-----SNYSCLSSRLRVSAFWQPNRHFRCQVQFGLSEEDKWPESGPKPTQN 116
QY 256 VSAEAWGRADCGFTSESQOQVLSATILYEILLGKATLYAVLVSAVLVMAVKKRDS 312
DB 117 ISAEAWGRADCGITTSASYQOQVLSATILYEILLGKATLYAVLVSTLVMAVKKRNS 173

RESULT 5
TCB2_MOUSE STANDARD; PRT; 173 AA.
AC P01851;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE T-CELL RECEPTOR BETA-2 CHAIN C REGION.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B10.A;
RX MEDLINE; 84270704.
RA Gascoigne N.R.J., Chien Y., Becker D.M., Kavalier J., Davis M.M.;
RT "Genomic organization and sequence of T-cell receptor beta-chain
RT constant- and joining-region genes.";
RL Nature 310:387-391(1984).
RN [2]
RP SEQUENCE FROM N.A. (CLONE 2C).
RC STRAIN-BALB.B;
RX MEDLINE; 84245824.
RA Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA Tonegawa S.;
RT "Complete primary structure of a heterodimeric T-cell receptor
RT deduced from cDNA sequences.";
RL Nature 309:757-762(1984).
CC -!- MISCELLANEOUS: CLONE B10.A WAS ISOLATED FROM A CYTOTOXIC T
CC LYMPOCYTE.
CC -!- MISCELLANEOUS: CLONE 2C WAS ISOLATED FROM A CYTOTOXIC T
CC LYMPOCYTE.
DR PIR; A02134; RMSBSC.
DR PFAM; PF00047; 1g; 1.
KW T-cell; Receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 146 C REGION.
FT TRANSMEM 147 168 CYTOPLASMIC TAIL.
FT DOMAIN 169 173
FT VARIANT 50 50 K -> R (IN CLONE 2C).
FT VARIANT 70 70 Y -> H (IN CLONE 2C).
FT SEQUENCE 173 AA; 19297 MW; A5458149614CF295 CRC64;
SQ

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Query Match 43.9%; Score 731; DB 1; Length 173;
Best Local Similarity 78.5%; Pred. No. 9.4e-55;
Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;

QY 136 EDLKNVPPEVAVFPSEAEISHTQKATLVCLATGTFYDPDHVELSWWVNGKEVHSGVSTDP 195
DB 1 EDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDP 60
QY 196 QPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQFGLSENDEWTDQRAKPTQI 255
DB 61 QAYKE-----SNYSCLSSRLRVSAFWQPNRHFRCQVQFGLSEEDKWPESGPKPTQN 116
QY 256 VSAEAWGRADCGFTSESQOQVLSATILYEILLGKATLYAVLVSAVLVMAVKKRDS 312
DB 117 ISAEAWGRADCGITTSASYQOQVLSATILYEILLGKATLYAVLVGLVMAVKKNS 173

RESULT 6
TVB2_HUMAN STANDARD; PRT; 133 AA.
AC P04435;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-CELL RECEPTOR BETA CHAIN V REGION CTL-L17 PRECURSOR.
GN TCRB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86276770.
RA Leiden J.M., Fraser J.D., Strominger J.L.;
RT "The complete primary structure of the T-cell receptor genes from an
RT alloreactive cytotoxic human T-lymphocyte clone.";
RL Immunogenetics 24:17-23(1986).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A HUMAN CYTOTOXIC
CC T-LYMPHOCYTE THAT IS T3+, T4+, T8+.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M15564; AAA61027.1; -.
DR PIR; A02001; RWHU7B.
DR PFAM; PF00047; 1g; 1.
KW T-cell; Receptor; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 133 T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT L17.
FT DOMAIN 22 114 V SEGMENT.
FT DOMAIN 115 118 D SEGMENT.
FT DOMAIN 119 133 J SEGMENT.
FT CARBOHYD 30 30
FT CARBOHYD 37 37
FT DISULFID 42 111
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14999 MW; 21030818D18D341F CRC64;

Query Match 26.0%; Score 433; DB 1; Length 133;
Best Local Similarity 62.2%; Pred. No. 7.9e-30;
Matches 84; Conservative 15; Mismatches 34; Indels 2; Gaps 1;

QY 1 MGTSLLCWALCLLGADHTGACVSTPSNKKYTKGDKVELRCDPTSGHTALYVWRQSLGQ 60
DB 1 MGTSLLCWALCLLGADHTGCVSQNPENHTKRGQNTFRCDPTSEHRLYVTRQLGQ 60

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KW T-cell; Receptor; Signal.
FT SIGNAL 1 20
FT CHAIN 21 - 135
FT 3H.25.
FT DOMAIN 21 115
FT DOMAIN 116 118
FT DOMAIN 119 135
FT DISULFID 42 111
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15123 MW; C0FF1DDACF37E76D CRC64;

Query Match 15.0%; Score 249.5; DB 1; Length 135;
Best Local Similarity 42.2%; Pred. No. 2.2e-14;
Matches 57; Conservative 16; Mismatches 59; Indels 3; Gaps 1;

QY 1 MGRLLCWAALCLLGGADHTGAGSVQPSNKKVTEKGDVELRCDPISGHTALYWRQSLGQ 60
Db 1 MATRLCYTVCLLGARILNSKVQTPRYLVKGGQKAKMRCIPEKGHVVFVWYQNNKN 60

QY 61 GPFFLIYFGTGAAADSGPLNDRFFFAVRPEGSVSTLKIQRTQGGDSAAAYLRAGVAGWSS 120
Db 61 EFRLINQVQVLOQIDMTKRFSAECPNSPCSLQISQSEAGDSALYLCASSLFGTSD 120

QY 121 YNEQYFGPGTRLTVL 135
Db 121 YT---FGSGTRLVLI 132

RESULT 10
TVB5_MOUSE STANDARD; PRT; 122 AA.
AC P04213;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-CELL RECEPTOR BETA CHAIN V REGION C5 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85036636.
RA Patten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT "Structure, expression and divergence of T-cell receptor beta-chain
variable regions.";
RL Nature 312:40-46(1984).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A T-HELPER CLONE.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X01643; CAA25800.1; -
CC PIR; A02007; RWSLNB.
CC PFAM; PF00047; Ig; 1.
CC T-cell; Receptor; Signal.
KW SIGNAL 1 21
FT CHAIN 22 136
FT DOMAIN 22 116
FT DOMAIN 117 120
FT DOMAIN 121 136
FT DISULFID 45 113
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15369 MW; F74D0C0414088D02 CRC64;

T-CELL RECEPTOR BETA CHAIN V REGION LB2.
V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.

Query Match 10.8%; Score 180.5; DB 1; Length 136;
Best Local Similarity 32.6%; Pred. No. 1.4e-08;
Matches 45; Conservative 25; Mismatches 63; Indels 5; Gaps 3;

QY 1 MGRLLCWAALCLLGGADHT---GAGVSQTPSNKKVTEKGDVELRCDPISGHTALYWRQS 57
Db 1 MNKWVFCWVTLCLLAVETHGDDGIITQPKFLIQEGQKTLKCCQNFNDHTMYWYRQD 60

QY 58 LGGQPEFLIYFGTGAAADSGPLNDRFFFAVRPEGSVSTLKIQRTQGGDSAAAYLRAGVAG 117
Db 61 SGKGLR-LIYYSITENDLQKGLDSEGYDASREKKSFSILTVTSQAKNMTVFLCAS-SIR 118

QY 118 WSSYNEQYFGPGTRLTVL 135
Db 119 LSAETLYFGSGTRLTVL 136

RESULT 12
LAC2_RAT STANDARD; PRT; 104 AA.
ID LAC2_RAT
AC P20767;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG LAMBDA-2 CHAIN C REGION.
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SQ SEQUENCE 133 AA; 14986 MW; 73E8E9EBF6F85290 CRC64;

Query Match          9.9%; Score 165; DB 1; Length 133;
Best Local Similarity 31.1%; Pred. No. 2.8e-07;
Matches 42; Conservative 22; Mismatches 69; Indels 2; Gaps

Qy 1 MGTRELLCWAALCLLGADHTGAGVSGTSPNKTVEKGDKVELRCDPISGHTALYWRQSLGQ 60
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Db 1 MSCRELLLYVSLCVETALMNTKTKTQSPRYLILGRA-NKSLCEQHLGHNNMYWKQSAEK 59
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Qy 61 GPFLYIFQGTGAADSGLPNDRRFFAVRPEGSYSTLIQRTQEGDSSAAYLRAGVAAGWS 120
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Db 60 PPELMFLYLNKLQIRNETVPS-RFIEPCPDSSKLLHLISAVDPEDSAVYFCASSHGGVS 118
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Qy 121 YNEQYTGPGTRLTVL 135
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Db 119 GNTLYFGESRLIVV 133
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :

RESULT 14
TVB8_MOUSE ID TVB8_MOUSE STANDARD; PRT; 130 AA.
AC P06321;
CD
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-CELL RECEPTOR BETA CHAIN V REGION A20.2.25 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [..]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86068062.
RT Morinaga T., Fotedar A., Singh B., Wegmann T.G., Tamaoki T.;
RT "Isolation of cDNA clones encoding a T-cell receptor beta-chain from
RT a beef insulin-specific hybridoma";
RL Proc. Natl. Acad. Sci. U.S.A. 82:8163-8167(1985).
DR PIR; A02005; RWSM20.
DR PFAM; PF00047; Ig; 1.
KW T-cell; Receptor; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 >130 T-CELL RECEPTOR BETA CHAIN V REGION
FT FT 22 112 A20.2.25.
FT DOMAIN 22 112 V SEGMENT.
FT DOMAIN 113 115 D SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT CARBOHYD 36 36 POTENTIAL.
FT CARBOHYD 75 75 POTENTIAL.
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14732 MW; 6721EC70DC64BEDB CRC64;

Query Match          9.7%; Score 161.5; DB 1; Length 130;
Best Local Similarity 30.4%; Pred. No. 5.3e-07;
Matches 41; Conservative 23; Mismatches 66; Indels 5; Gaps

Qy 1 MGTRELLCWAALCLLGADHTGAGVSGTSPNKTVEKGDKVELRCDPISGHTALYWRQSLGQ 60
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Db 1 MSCRELLLYVSLCVETALMNTKTKTQSPRYLILGRA-NKSLCEQHLGHNNMYWKQSAEK 59
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Qy 61 GPFLYIFQGTGAADSGLPNDRRFFAVRPEGSYSTLIQRTQEGDSSAAYLRAGVAAGWS 120
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Db 60 PPELMFLYLNKLQIRNETVPS-RFIEPCPDSSKLLHLISAVDPEDSAVYFCASSHGE 115
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Qy 121 YNEQYTGPGTRLTVL 135
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :
Db 116 NTEVFEGKGTLLIW 130
    | | | | : | | | : | | | : | | | : | | | : | | | | | | :

RESULT 15
I141_HUMAN ID I141_HUMAN STANDARD; PRT. 213 AA
IT

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	181	10.9	214	11	Q9RIA5		Q9rla5 mus musculus
2	177.5	10.7	259	13	Q90530		Q90530 ginglymosto
3	166	10.0	268	13	Q90524		Q90524 ginglymosto
4	165.5	9.9	267	13	Q90529		Q90529 ginglymosto
5	161	9.7	257	13	Q90536		Q90536 ginglymosto
6	156.5	9.4	237	11	Q9RIA4		Q9rla4 mus musculus
7	155.5	9.3	452	13	Q90568		Q90568 ginglymosto
8	154	9.3	684	13	Q90544		Q90544 ginglymosto
9	145.5	8.8	509	11	Q08907		Q08907 mus musculus
10	145.5	8.7	137	4	Q9UDR1		Q9udr1 homo sapien
11	145.5	8.7	333	7	Q31522		Q31522 poecilia re
12	145.5	8.7	509	11	Q9WTF4		Q9wtf4 mus musculus
13	145	8.7	345	7	P79599		P79599 rattus norv
14	142.5	8.6	361	7	O62896		O62896 ictalurus p
15	142	8.5	348	7	O46875		O46875 rattus norv
16	141.5	8.5	237	13	Q90545		Q90545 ginglymosto
17	141.5	8.5	346	7	O78088		O78088 rattus norv
18	141.5	8.5	367	7	P79589		P79589 rattus norv
19	141	8.5	296	7	Q31274		Q31274 rattus norv

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Db 96 FTGSGTKL-----BIKRADAAPTIVFPSPSEQLT-SGGASVVCFLNNEYPKIDINVKWKI 150
QY 183 NGKEVHSGV--STDQPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQ 232
Db 151 DGSERQGVNLNWDQDSK-----DSTYSMSSTLTITKDEYER-HNSYTCE 195

RESULT 2
Q90530
ID Q90530 PRELIMINARY; PRT; 259 AA.
AC Q90530;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
RN [1]
RN SEQUENCE OF 1-235 FROM N.A.
RP TISSUE=SPLEEN;
RC MEDLINE: 95183140.
RA Greenberg A.S.; Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=SPLEEN;
RC Greenberg A.S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U18687; AAB48358.1; -.
DR HSSP; P01842; 7FAB.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 259
SQ SEQUENCE 259 AA; 28245 MW; 07F9860A92318B6E CRC64;

Query Match 10.7%; Score 177.5; DB 13; Length 259;
Best Local Similarity 27.3%; Pred. No. 7.7e-09;
Matches 63; Conservative 30; Mismatches 105; Indels 33; Gaps 10;

QY 21 AGVSQTPSNKVTEKGDVLR-----DPISGHTALYWRQSLGQGFPEFLIYFGTGAAD 75
Db 19 ARVDQTPRSVTKETGESLTINCLRDASVALGHTC--WFRKKGSTKE----- 64

QY 76 DSGLPNDRFPAVRPEGVSILKIQTEQGSAAAYLRAGVAAGHSSYNEQYF-----GPGT 130
Db 65 ENISPGGRY--VFVNVSQNLNLDLTVEDGGTYRGCGSLYNWCSCETDVLPLAACGAGT 122

QY 131 RLTVLEDLKNVFPPEVAFPEPSAEISHTOKATLVCLATGYDPDHVELSWWNGKEVHSG 190
Db 123 AVTVNPGIP-PSPIVSLLSHSAEEQANRFVQLVCLISGYYPENIAVSWQKNTKITSG 181

QY 191 VSTDQPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQVYGLSN 241
Db 182 FAT-TSPVK--TSSND--FSCASLLKVPLOEWSR-GSVYSCQVSHSATSN 226

RESULT 3
Q90524
ID Q90524 PRELIMINARY; PRT; 268 AA.
AC Q90524;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR (FRAGMENT)
OS Ginglymostoma cirratum (Nurse shark).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
RN [1]
RN SEQUENCE OF 1-240 FROM N.A.
RP TISSUE=SPLEEN;
RC MEDLINE: 95183140.
RA Greenberg A.S.; Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=SPLEEN;
RC Greenberg A.S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U18680; AAB48352.1; -.
DR HSSP; P01842; 7FAB.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 268
SQ SEQUENCE 268 AA; 29579 MW; 0CDE524DD6E9FDC4 CRC64;

Query Match 10.0%; Score 166; DB 13; Length 268;
Best Local Similarity 26.1%; Pred. No. 9.7e-08;
Matches 74; Conservative 38; Mismatches 121; Indels 50; Gaps 13;

QY 21 AGVSQTPSNKVTEKGDVLRCDPISGHTAL---YWRQSLGQGFPEFLIYFGTGAADDS 77
Db 19 ARVDQTPQBITKETGESLSINCLVRLSDNCALFSTYNNRKGSTNEETISKGG----- 71

QY 78 GLPNDRFFPAVRPEGVS-TLKIQTREQDSAAAYLRAGVAAGHSSYNEQYF-----YFGP 128
Db 72 -----RYVETVNSGSKSFLRLNLDLTVEDSGTYRCKYVRKNW-AYDCGLELDWIYVVG 125

QY 129 GTRLTVLEDLKNVFPPEVAFPEPSAEISHTOKATLVCLATGYDPDHVELSWWNGKEVH 188
Db 126 GTGVTNPGIP-LSPPIVSLLSHSAEEQANRFVQLVCLISGYYPENIAVSWQKNTKIT 184

QY 189 SGVSTDQPLKEQPALNDSRYCLSSRLRVSAFWQPNRHFRCQVQVYGLSEND-----EW 244
Db 185 SGFAT-TSPVK--TSSND--FSCASLLKVPLOEWSR-GSVYSCQVSHSATSNQKKEIRS 238

QY 245 TODRAKPTQIVSAPAWGADCGFTSESYQQGVLSATILYEIL 287
Db 239 TSEIAVLLRDPVVEIWINK-----SATLVCEVL 267

RESULT 4
Q90529
ID Q90529 PRELIMINARY; PRT; 267 AA.
AC Q90529;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
RN [1]
RN SEQUENCE OF 1-243 FROM N.A.
RP TISSUE=SPLEEN;
RC MEDLINE: 95183140.
RA Greenberg A.S.; Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).

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[illegible]

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RESULT      5
Q90536
ID          AC          PRELIMINARY;      PRT;      257 AA.
AC          Q90536;
DT          01-NOV-1996 (TREMBLrel. 01, Created)
DT          01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT          01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE          NOVEL ANTIGEN RECEPTOR (FRAGMENT).
OS          Ginglymostoma cirratum (Nurse shark).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC          Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC          Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
[1]
RN          SEQUENCE OF 1-242 FROM N.A.
RP
RC          TISSUE=SPLEEN;
RX          MEDLINE; 95183140.
RA          Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA          Flajolet M.F.
RT          "A new antigen receptor gene family that undergoes rearrangement and
RT          extensive somatic diversification in sharks.";
RL          Nature 374:168-173(1995).
[2]
RN          SEQUENCE FROM N.A.
RP
RC          TISSUE=SPLEEN;
RA          Greenberg A.S.;
RA          Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RL          EMBL; U18693; AAB48364.1; -.
DR          HSSP; P01842; 7FAB.
DR          INTERPRO; IPR000495; -.
DR          INTERPRO; IPR003006; -.
DR          PFAM; PF000047; 1g; 2.
DR          PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR          NON_TER      257
SQ          SEQUENCE      257 AA; 28083 MW;  BAD019A99D0BC491 CRC64;

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Query Match 9.78; Score 161; DB 13; Length 257;

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Best Local Similarity 27.0%; Pred. No. 2.7e-07;
Matches 63; Conservative 31; Mismatches 105; Indels 34; Gaps 10;

QY 23 VSQTPSNKVTGKGDVLRCDPISGHTAL---YVWROS LGQGPEFLIYFOGTGAADD SGL 79
   ||| : : : : : ||| : : : : :
Db 21 VDQTPRSVTRTGESLINCVLREAPYALSKTCWRKKS GSTNQSISKGG----- 71

QY 80 PNDREFF-AVRPEGVS TLKIQRTQGGSAAYLRAGVAGWSYNEQ-----YFGP 128
   || : : : : : ||| : : : : :
Db 72 --RYVETVNSELKSFSLRINDLVEDGGTY-ROGAWPSWNSHGCSGDWAVGGAYAAVD 127
   ||| : : : : : ||| : : : : :

QY 129 GTRLTVLEDLKNVPPVAVPEPEAEISHQKATLVCLARGFYDPDHVLSWVNGKEVH 188
   ||| : : : : : ||| : : : : :
Db 128 GTATVAVPGIP-PPPIVSLLSHSAETEORANRFVQLVCLISGYYPENIAVSWQKNTKIT 186

QY 189 SGVSTDPOPLKEQPALNDSRYCLSLRSLRYATFWQNPRNHFRCOVQYGLSEN 241
   || : : : : : ||| : : : : :
Db 187 SGFAT-TSPVK--TSSND--FSCASLLKVLQPEWSR-GSVYSCOVSHSATSSN 233

RESULT 6
Q9RI1A4 PRELIMINARY; PRT; 437 AA.
AC Q9RI1A4
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TremBLrel. 14, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF152372; AAD40243.1;
DR INTERPRO: IPR000495;
DR INTERPRO: IPR003006;
DR PRAM: PF000047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 9.4%; Score 156.5; DB 11; Length 437;
Best Local Similarity 27.1%; Pred. No. 1.5e-06;
Matches 58; Conservative 33; Mismatches 98; Indels 25; Gaps 10;

QY 25 QTPSNKVTGKGDVLRCDPISGHT---ALYVWRQSLGQGPEFLIYFOGTGAADD SGLP 80
   ||| : : : : : ||| : : : : :
Db 4 QESGGVLKPGSLKLSL-ARSGTFFSYANSWVRQPEKLEWVASPSSGGIYYTDSV 62

QY 81 NDRFAVR-PEGVSVSTLKIQTQEGDSNAYLRAGVAGWSYNEQYFGPGRITVLEDLK 139
   || : : : : : ||| : : : : :
Db 63 KGRETIYKDKDRNLTLSQMSLSRSDTANYFCAR----GDYS-AYMGPGTLTVT--SAA 114

QY 140 NVFPEVAVPEPSAEISHTQKATLVCLATCFYDPDHVLSWVNGKEVHSGVSTDPOPLK 199
   ||| : : : : : ||| : : : : :
Db 115 KTTSPSYVPLAPGSAQTNSM-VTLGCLVKVGYFEPVTVTW--NSGSLSSGVHTFP---- 167

QY 200 EQPALNDSRYCLSLRSLRYATFWQNPRNHFRCOV 233
   ||| : : : : : ||| : : : : :
Db 168 --AVLQSDLYTLSSSVTPSPSTW--PSETVTCNV 197

RESULT 7
Q90368 PRELIMINARY; PRT; 252 AA.
ID Q90568
AC Q90568;

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DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE NOVEL ANTIGEN RECEPTOR (FRAGMENT).
 OS Ginglymostoma cirratum (Nurse shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
 OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
 RN [1]
 RP SEQUENCE OF 1-239 FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 95183140.
 RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
 RA Flajnik M.F.
 RA "A new antigen receptor gene family that undergoes rearrangement and
 RT extensive somatic diversification in sharks."
 RL Nature 374:168-173(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 95183140.
 RA Greenberg A.S.,
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U18725; AB42387.1; -.
 DR HSSP; P01842; 7FAB.
 DR INTERPRO; IPR000495; -.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 252 252
 SQ SEQUENCE 252 AA; 27356 MW; 117F2225B2E17EDF CRC64;

Query Match 9.3%; Score 155.5; DB 13; Length 252;
 Best Local Similarity 27.6%; Pred. No. 8.6e-07;
 Matches 64; Conservative 31; Mismatches 102; Indels 35; Gaps 11;

QY 23 VSQTPSNKYTEKGDVLRCDPSGHTALYWRQSLGQGPFLI----YFQGTGAADSG 78
 DB 21 VLQTPSAVTKETGSLTINC-----VLRDSPQSLAGTCWYFTRSGSRSEER 66
 QY 79 L-PNDRFFAVRPEGSVS-TLKIQTQEGDGAAYLRAGVAAGWS-----YNEQYFGPG 129
 DB 67 IRAGRVVEIVNSGSKFSKLINDLTVEDGGTY-RCVAGTHSGCALCSFIQIETCGEG 125
 QY 130 TRLVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFPYDPHVELSWV 189
 DB 126 TAVTVNPGIP-PSPIIVSLLHSATEEQANRFVQLVCLISGYYPENIAVSWQNTKTITS 184
 QY 190 GVSTDPOPLKEQPALNDSRYCLSLRLVSATFWQNPENHFRCCOVQVGLSEN 241
 DB 185 GFAT-TSPVK--TSSND--FSCASLHKVLPQWNSR-GSVYSCQVSHSATSSN 230

RESULT 8
 ID Q90544 PRELIMINARY; PRT; 684 AA.
 AC Q90544;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE NOVEL ANTIGEN RECEPTOR PRECURSOR.
 OS Ginglymostoma cirratum (Nurse shark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
 OC Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 95183140.
 RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
 RA Flajnik M.F.
 RA "A new antigen receptor gene family that undergoes rearrangement and
 RT extensive somatic diversification in sharks."

RL Nature 374:168-173(1995).
 DR EMBL; U18701; AB48195.1; -.
 DR INTERPRO; IPR000495; -.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; ig; 6.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.
 SQ SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6DFD CRC64;

Query Match 9.3%; Score 154; DB 13; Length 684;
 Best Local Similarity 22.8%; Pred. No. 4.7e-06;
 Matches 64; Conservative 41; Mismatches 110; Indels 56; Gaps 12;

QY 23 VSQTPSNKYTEKGDVLRCDPSGHTALYWRQSLGQGPFLIYFQGTGAAD 75
 DB 21 VDQTPRSVAKAEQVLTINCVLRGANYELAKGSTC--WYRKKS-----SKVE 66
 QY 76 DSCLPNDRFFAVRPEGSVS-TLKIQTQEGDGAAYLRAGVAAGWSYNEQYF----- 126
 DB 67 ESTTKGRYVETVNSGSKFSKLINDLTIEDAGDYR---CAAEAAADCMYGVCTIYPF 122
 QY 127 ----GPGTRLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFPYDPHVELSWV 182
 DB 123 SGACGSGTAVTTPGIP-PSPIIVSLLHSATEEQANRFVQLVCLISGYYPENIAVSWQ 181
 QY 183 NGEVHSGVSTDPQLKEQPALNDSRYCLSLRLVSATFWQNPENHFRCCOVQVGLSEN 242
 DB 182 NTKTITSGPAT-TSPVK--TSSND--FSCASLHKVLPQWNSR-GSVYSCQVSHSATSSN 235
 QY 243 E-----WTQDRAPVTQIVSAPAWG 262
 DB 236 RKEIRSTSEIALLRDPVTVEEIWIDKSLTLCVCEVLTSTVSAG 276

Query Match 8.8%; Score 146.5; DB 11; Length 509;
 Best Local Similarity 22.4%; Pred. No. 1.6e-05;
 Matches 95; Conservative 58; Mismatches 132; Indels 139; Gaps 24;

QY 1 MGTTRLLC--WAALCL-LGADHTGAGVSTPSPNKYTEKGDVLRCD-----PISGHTALY 52
 DB 11 LGPLLLCLLLSACFCTGATGTETVKVTPPEKSVSVAAGDSTILNCTVTSLLPVG---PIR 67

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QY 53 WYRQSLGQGPPELIYFQGTGA-----ADDSGLPNDRFFAVR-----PE--GSYSTLKI 98
Db 68 WYR---GVQSRLLIYSFTGEHFPVRNVSDTKRNNMDFSIRISNVPEDAGTICYKVF 124
QY 99 QR-TEQDGAAYLRACVAAGWSSYNEQYFGPGTGLTIVLEDLKNNVPEVAVPEPSEAEIS 157
Db 125 QRGSSSEPD-----EIQSGGTEYV---LAKSPPEVS--GPADRGIP 163
QY 158 HTQKATLVCLATGFFPDHVELSWVNGKEVH-----SG-----VSTDPOPLKEQPA 203
Db 164 -DQVNFCTKSHGFSRNTLTKWFKDQELHPLFTVNFSGKNVSYNISSTVRVVLNSMD 222
QY 204 LNSRYC-----LSSRLRVSAT--FWGNP-----RNHFRQC----- 232
Db 223 VNSKVCCEVAHITLDRSPGLRGIANLNFIRVSTFKVTCQPTSMNQVNLICRAERFYPE 282
QY 233 -VOFYGLSENDEWTDQRAKPVTO-----IVSAEANGRADCGFT----- 269
Db 283 DLQIWLNGVNSRNDTPKNLTKNTDGTNYTSLFLVNSSA-HREDVVFTQVKKHQQPA 341
QY 270 -----SESYOQGVL-----SATLYEILIG---KATLYAVLYSALVLMAMWKRK 310
Db 342 ITRNHTVGLAHSSDQGSQCTPFGNATHNWNVFIGVACALLVVLLMAALYLIRIKQK 401
QY 311 DSRG 314
Db 402 KAKG 405

RESULT 10
Q9UDR1
ID Q9UDR1 PRELIMINARY; PRT; 137 AA.
AC Q9UDR1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE T-CELL RECEPTOR GAMMA CHAIN, TRGV9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99063792.
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Arnett C., Wohlmann P., Le T.;
RT "The sequence of Homo sapiens BAC clone RP11-121A8.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006033; RAD15557.1;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; ig; 1.
KW Receptor.
SQ SEQUENCE 137 AA; 15184 MW; BLF09F63D3671609 CRC64;
```

Query Match 8.7%; Score 145.5; DB 4; Length 137;
Best Local Similarity 33.3%; Pred. No. 3.2e-06;
Matches 44; Conservative 19; Mismatches 59; Indels 17; Gaps 7;

```
QY 10 ALCLLGADHTGAGVSGTPSNKTEKGVKDELRCDFISG-----HTALYWRQSLGQGPFL 65
Db 15 ALCVYGAGH----LEQPOISSKTLKSTARLEC-VVSGITISATSVYWRERPEGVIOFL 69
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QY 66 --IYFGQTGAADDSGLPNDRFFAVR-PBGSVSTLKIQTQEQDGAAYLRACVAAGWSSYN 122
Db 70 VSIISYDGT-VKESGIPSGKEVDRIPTSTLTITHNVEKODIATY----YCALWEVHS 124
QY 123 EYFGPGTGLTV 134
Db 125 SRQFEPHSINW 136

RESULT 11
Q31522
ID Q31522 PRELIMINARY; PRT; 333 AA.
AC Q31522
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE MHC CLASS IA (FRAGMENT).
OS Poecilia reticulata (Guppy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
OC Atherinomorpha; Cyprinodontiformes; Cyprinodontidae; Poeciliidae;
OC Poecilia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96128251.
RA Sato A., Figueroa F., O'Huigin C., Reznick D.N., Klein J.;
RT "Identification of major histocompatibility complex genes in the
RT guppy, Poecilia reticulata.";
RL Immunogenetics 43:38-49(1996).
DR EMBL; Z54085; CAA90791.1;
DR INTERPRO; IPR001039;
DR INTERPRO; IPR003006;
DR PFAM; PF00047; ig; 1.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1
SQ SEQUENCE 333 AA; 37165 MW; D9C042B504B8014D CRC64;

Query Match 8.7%; Score 145.5; DB 7; Length 333;
Best Local Similarity 22.1%; Pred. No. 1.1e-05;
Matches 63; Conservative 34; Mismatches 81; Indels 107; Gaps 10;

QY 54 YRQSLGQGPPELIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQTQEQDGAAYLRAG 113
Db 113 YTFQGYDGDFFSVF-----DLKTESWTPVTEAVVTHKWDNDK-----G 152
QY 114 VAAGWSSYNEQ-----YFGPGTGLTVLEDLKNNVPEVAVPEPSEAEISHTOKATLV 165
Db 153 LNAWGVNLTQNCPEWLKKYNYGR-----SSLMTVPVPSVSL-----LQMTSSSPVS 200
QY 166 CLATGFYPDHVELSWVNGKEVSGVSTDPQLKEQPALNDSRYCLSSRLRVSATFWQNP 225
Db 201 CYATGFYFNRAEMLWRKGVETHDGVKGV-----EILPNDGTFQMSVELTSLA----- 249
QY 226 RNHFRQVQFYGLSENDEWTDQRAKPVTOIVSAEANGRADCGFTSESYQQGVLSATILYE 285
Db 250 -----SEDTWKYDCVFOGLSGVDKDLV----- 270
QY 286 ILLGKA-----TLYAVLV---SALVLMAMWKRKDSR 313
Db 271 IPLDKANIKTNAGNSLALITIVAVVLTISAVIVILVLRKKAK 315

RESULT 12
Q9WTN4
ID Q9WTN4 PRELIMINARY; PRT; 509 AA.
AC Q9WTN4
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BIT.
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GN BIT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=BRAIN;
 RA Sano S.;
 RT "Mouse type III BIT."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB018194; BAA76555.1;
 DR INTERPRO; IPR000495;
 DR INTERPRO; IPR003006;
 DR PFAM; PF00047; ig; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 509 AA; 55986 MW; CF3A6EC9404C14CF CRC64;
 Query Match 8.7%; Score 145.5; DB 11; Length 509;
 Best Local Similarity 22.1%; Pred. No. 2e-05;
 Matches 92; Conservative 56; Mismatches 144; Indels 125; Gaps 22;
 QY 1 MGTLLC--WAALCL-LGADHTGAGYSQTPSNKVTEKGDVELRCD-----PISGHTALY 52
 DB 11 LGPILLCLLSASCFCTGATGKELKVTQPEKSVSVAAGDSTVNLCTLTLLPVG----PIR 67
 QY 53 WYRQSLGQGEFFLIYFGTGA-----ADDSGLPNDRFFAVRPEGSVSTLKIQTREQD 105
 DB 68 WYR--GVGFSRLIYSFAGEYVPIRNVSDTTKRNMDFSI-----ISNVTPAD 115
 QY 106 SAAYLRAGVAGHSSYN-EQYFGCTRLTVLEDLKNVFPPEAVFPSPAEISHTOKATL 164
 DB 116 AGIYCYVKFKGSEPDTEIQSGGTEYV--LAKPSPPEVS--GPADRGIP-DQKVF 169
 QY 165 VCLATGYPDHVELSMVNGKEVH-----SG-----VSTDQPLKEQPALNDSRYC 210
 DB 170 TCKSHGFSRNITLKFWDQQLHPLTTPVNPCKVNSVNISSVTRVNLSDVNSKVIC 229
 QY 211 -----LSSRLVSATF--WONPRN-----HFRQ-----VQFYL 238
 DB 230 EVAHITLDRSPLRGIANLSNFIRVSTVKVTQOSPTSMQVNLTCRAERFYPEDLQIWL 289
 QY 239 SENDWTQDRAKPTQ-----IVSAEAWGRADCGT----- 269
 DB 290 ENGNSRNDTPKRLTNKNDGTNYWTSFLVNSSA-HREDVVFVCQVKHQDQPAITRNHTV 348
 QY 270 ---SESYQGVGL-----SATILYEILG---KATLYAVLVSAVLVLMAMVKRKRDSRG 314
 DB 349 LGFAHSSDQSGMOTFPDNNATHWNVFIGVGACALLVLLMAALVLLRIKQKAKG 405
 RESULT 13
 ID P79599 PRELIMINARY; PRT; 345 AA.
 AC P79599; Q95564;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE MATURE ALPHA CHAIN OF MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I
 DE ANTIGEN (FRAGMENT).
 GN RT1.A1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RT1.0; TISSUE=SPLEEN;
 RA Joly E., Le Rolle A.F., Gonzalez A.L., Mehling B., Stevens J.,
 RA Coadwell W.J., Huenig T., Howard J.C., Butcher G.W.;
 RL Curr. Biol. 0:0-0(1999).
 DR EMBL; X90373; CAA62023.1;
 DR HSSP; P01900; 1BII.
 DR INTERPRO; IPR000495;
 Query Match 8.6%; Score 142.5; DB 7; Length 361;
 Best Local Similarity 25.1%; Pred. No. 2.4e-05;
 Matches 51; Conservative 32; Mismatches 73; Indels 47; Gaps 7;
 QY 118 WSSYNE-----QYFGCTRLTVLEDLKNVFPPEAVFPSPAEISHTOKATLYCLAT 169
 DB 305 GAVVAVVRKRRTGG 320

DR INTERPRO; IPR001039;
 DR INTERPRO; IPR003006;
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC-I; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW MHC.
 FT NON_TER 1
 SQ SEQUENCE 345 AA; 39221 MW; 9A28E9E36993A7C8 CRC64;
 Query Match 8.7%; Score 145; DB 7; Length 345;
 Best Local Similarity 22.8%; Pred. No. 1.3e-05;
 Matches 72; Conservative 56; Mismatches 104; Indels 84; Gaps 16;
 QY 25 QTPSNKVTEKGDVELR-----CDPISGHTALYVWYROSUGOGPE 63
 DB 63 ETQNAKENEQVYRVLDTRLRGYYNQSEGSHTIQEMYCDVCGSLRGTRQDAYDGRD 122
 QY 64 FLIYFQG--TGAADDSGLPNDRFFAVRPEGSVSTLKIQTREQDS--AAYLRAGVAGHSS 120
 DB 123 YIALNEDLKTWAAD-----FAAQ---ITRNKWERARYAERLRLAYLQ-GTCVEWL- 168
 QY 121 YNEQYFGCTRLTVLEDLKNVFPPE--VAVFEPSEAEISHTOKATLYCLATGFFPDHVEL 178
 DB 169 --RRYLELGKETLLRSD-----PPKAHVTLHPRPEGV-----TLRCWALGFFPADISL 215
 QY 179 SMWVANGKEVHSGVSTDPOPLKEQPALNDSRYCLSSRLVSATFMQNPENHFRPCQVQFYL 238
 DB 216 SWQLNGED----LTQDMELVETRPA-GDGTQKQWASVVVPLGKEQN---YTCRVEHEGL 266
 QY 239 SENDWTQDRAKPTQIVSAEAWGRADCGFTSESYQGVGLSATILYEILCKATLYAVLV 298
 DB 267 PE-----PLSQ-----RWEPSSLTDSN---METTVIYVVLGAVATIAAII 304
 QY 299 SALVLMAMVKRKRDSRG 314
 DB 305 GAVVAVVRKRRTGG 320
 RESULT 14
 ID O62896 PRELIMINARY; PRT; 361 AA.
 AC O62896;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE MHC CLASS I ALPHA CHAIN.
 GN ICPU-E7.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Siluriformes; Ictaluridae; Ictalurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Antao A.B., Chinchar V.G., McConnell T.J., Miller N.W., Clem L.W.,
 RA Wilson M.R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053549; AAD08650.1;
 DR INTERPRO; IPR001039;
 DR INTERPRO; IPR003006;
 DR PFAM; PF00047; ig; 1.
 DR PFAM; PF00129; MHC-I; 1.
 DR PRODOM; PD000050; -. 1.
 KW MHC.
 SQ SEQUENCE 361 AA; 40914 MW; AB686B3F5A9CC1E6 CRC64;

Search completed: October 11, 2000, 06:30:06
Job time: 1285 sec

Db 178 WKNYLEKECIEIWLQXYVGYGR-----ETLBRKVPPTASVFQBEES-----SPEVYCHAT 226
Qy 170 GFYDPHVELSWNGKVKHSGVSDPDLKQEPALNDSRYCLSSRLRVSATFWQNPENHF 229
Db 227 GFFPKTYMITWQKDGEDVHEDVE-----LRETLPNQDGTQKRSILTVSAEDLQ--KHTY 279
Qy 230 RCOVQFGLSENDEWTDRAKPTQIVSAEAWGRADCGFTSESVOQGVLSATILYEILLG 289
Db 280 TCVIQHSSLE-----KEMVLPVSE-----RRILNPGGGGVVLIGIIVG 318
Qy 290 KATLYAVLVLSALVLMAMVKRKDS 312
Db 319 VVAALLVLVAVVAGIVVWKKKNS 341

RESULT 15

O46875 PRELIMINARY; PRT; 348 AA.
AC O46875;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
DE MHC CLASS IB ALPHA CHAIN PRECURSOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PVG.R19; TISSUE-SPLEEN;
RA Leong L.Y.W., Deverson E.V., Joly E., Butcher G.W.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13850; CAA74192.1; -.
DR HSSP; P01900; 1B11.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR001039; -.
DR INTERPRO; IPR001064; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 1.
DR PFAM; PF00129; MHC_I; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal; MHC.
FT NON_TER 1 1
FT SIGNAL <1 3 POTENTIAL.
FT CHAIN 4 348 MATURE MHC CLASS IB ALPHA CHAIN.
SQ SEQUENCE 348 AA; 39108 MW; BD4C4D8880ED611E CRC64;

Query Match 8.5%; Score 142; DB 7; Length 348;
Best Local Similarity 25.9%; Pred. No. 2.5e-05;
Matches 75; Conservative 44; Mismatches 97; Indels 74; Gaps 15;

Qy 49 TALWYRQSLGQGPFLIYFGTGAADDGSL-----PNDRFFAVRPEGVSSTLKIQR 100
Db 83 TLLRYNQSEG-GSHTFQWMSGCDLGSGLRLCYEQSAVNGRDYIVLNE-----DLKT 135
Qy 101 TEQDQSAYL-----RAGVAAGWSSYNEQYFGPGTRLTVL-----EDLNVPPE- 145
Db 136 WTAADTAARTIRNKWDRAVRAERKAYLE-----GTCLESLLRYLELQKETLLRSPPKA 190
Qy 146 -VAVFESEAEISHTQKATLVCLATGYPDHVELSWNGKVKHSGVSTDPQPKQOPAL 204
Db 191 HVTLHPRPGDV-----TLRCWALGFYPAGISLTWOLNGED----LTQDMELVETRPA - 239
Qy 205 NDSRYCLSSRLRVSATFWQNPENHFRQVQFYGLSENDEWTDRAKPTQIVSAEAWGRA 264
Db 240 GDGTFQKWSVVPPLGKEQN----YTCLVEHEGLPE-----PLTQ-----RW 277
Qy 265 DCGFTSESQGVLSATILYEILLGKATLYAVLVLSALVLMAMVKRKDSRG 314
Db 278 EPSPSTDSN----METNVYIIVLGVAIGAVIIAALVTIVR-KRRNTGG 322

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:06 ; Search time 15.62 Seconds
(without alignments)
687.378 Million cell updates/sec

Title: US-09-405-940-1

Perfect score: 1664

Sequence: 1 MGRLLCWAAALCLLGADHTG.....AVLSALVLMAMVKRKDSRG 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT:*

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12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1664	100.0	314	20 W99374	Human T-cell recep
2	1433	86.1	314	20 Y15229	Human receptor pro
3	1371	82.4	318	21 Y32208	Human receptor mol
4	1351	81.2	312	21 Y69988	Human receptor-ass
5	1273	76.5	345	21 Y69986	Human receptor-ass
6	1247.5	75.0	311	19 W47589	T-cell receptor be
7	1244	74.8	312	6 P50079	T-cell antigen rec
8	1244	74.8	312	7 P60471	Portion of a human
9	1230	73.9	312	15 R53145	T-cell antigen rec
10	1182	71.0	316	21 Y69999	Human receptor-ass
11	944	56.7	179	21 Y51069	Human TCRbeta prot
12	925.5	55.6	303	20 Y05403	Killer T-cell rece

13	907	54.5	177	21	Y51068	Human TCRbeta prot
14	896	53.8	306	6	P50252	Sequence of T-cell
15	883	53.1	314	20	Y05728	Mouse A1 T cell re
16	880	52.9	287	21	Y56077	HLA-A2/flu restric
17	880	52.9	287	21	Y57853	TCR beta chain and
18	880	52.9	306	6	P50344	Sequence encoded b
19	874.5	52.6	307	21	Y56059	HTLV-1 Tax/HLA-A2
20	874.5	52.6	307	21	Y56083	HTLV tax/HLA-A2 re
21	874.5	52.6	307	21	Y57859	TCR beta chain and
22	874.5	52.6	307	21	Y57868	TCR beta chain and
23	873.5	52.5	287	21	Y56079	Mouse H2-Dd/flu nu
24	873.5	52.5	287	21	Y56081	HLA-A2/HIV gag res
25	873.5	52.5	287	21	Y57855	TCR beta chain and
26	873.5	52.5	287	21	Y57857	TCR beta chain and
27	870	52.3	287	21	Y56056	HLA-A2/flu restric
28	870	52.3	287	21	Y57865	TCR beta chain and
29	870	52.3	305	21	Y56057	HLA-A2/flu restric
30	870	52.3	305	21	Y57866	TCR beta chain and
31	870	52.3	306	21	Y56061	HTLV-1 Tax/HLA-A2
32	870	52.3	306	21	Y56085	HTLV tax/HLA-A2 re
33	870	52.3	306	21	Y57861	TCR beta chain and
34	870	52.3	306	21	Y57870	TCR beta chain and
35	869.5	52.3	307	21	Y56086	HTLV tax/HLA-A2 re
36	869.5	52.3	307	21	Y57862	TCR beta chain and
37	868.5	52.2	293	7	P60238	Sequence of the be
38	868.5	52.2	293	10	P91815	Mammalian T lympho
39	868.5	52.2	293	18	W01532	Cytotoxic T lympho
40	868.5	52.2	293	21	Y50114	Murine cytotoxic T
41	827	49.7	391	17	R97659	Single chain T cel
42	811	48.7	150	21	Y51072	Human TCRbeta prot
43	736	44.2	173	21	Y51066	Murine TCRbeta pro
44	731	43.9	173	21	Y51067	Murine TCRbeta pro
45	621	37.3	146	21	Y51071	Murine TCRbeta pro

ALIGNMENTS

RESULT 1

W99374	ID	W99374	standard: Protein; 314 AA.
XX	AC	W99374;	
XX	DT	21-MAY-1999	(first entry)
XX	DE	Human T-cell receptor beta-like protein.	
XX	KW	T-cell receptor beta-like protein; antigen recognition; cancer;	
XX	KW	autoimmune disorder; antagonist; diagnosis.	
XX	OS	Homo sapiens.	
XX	PN	W09903995-A1.	
XX	PD	28-JAN-1999.	
XX	PF	17-JUL-1998; 98WO-US14598.	
XX	PR	18-JUL-1997; 97US-0897097.	
XX	PA	(INCY-) INCYTE PHARM INC.	
XX	PI	Corley NC, Hillman JL;	
XX	DR	WPI: 1999-132239/11.	
XX	DR	N-PSDB; X25736.	
XX	PT	New isolated T-cell receptor beta-like protein - used to develop	
XX	PT	products for the diagnosis and treatment of cancer or autoimmune	
XX	PT	disorders, e.g. AIDS, diabetes, infections or trauma	
XX	PS	Claim 1; Fig 1A-D; 69pp; English.	

XX This sequence represents a new purified T-cell receptor (TCR) beta-like
 CC protein (TCRLP). The TCRLPs are essential to the formation of a
 CC functional TCR and play a role in antigen recognition by T cells.
 CC The TCRLP polypeptides and polynucleotides appear to play a role in
 CC cancer and autoimmune disorders. The TCRLP and agonists can be used for
 CC treating cancer. TCRLP antagonists can be used for treating autoimmune
 CC disorders, e.g. AIDS, Addison's disease, adult respiratory distress
 CC syndrome, allergies, anaemia, asthma, atherosclerosis, bronchitis,
 CC cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis,
 CC dermatomyositis, diabetes mellitus, emphysema, erythema nodosum, atrophic
 CC gastritis, glomerulonephritis, gout, Graves' disease, hyperesinophilia,
 CC irritable bowel syndrome, lupus erythematosus, multiple sclerosis,
 CC myasthenia gravis, myocardial or pericardial inflammation, osteoporosis,
 CC osteoarthritis, pancreatitis, polymyositis, rheumatoid arthritis,
 CC scleroderma, Sjogren's syndrome, and autoimmune thyroiditis,
 CC complications of cancer, haemodialysis, and extracorporeal circulation,
 CC viral, bacterial, fungal, parasitic, protozoal, and helminthic infections
 CC and trauma. The products can also be used for detection, diagnosis and
 CC drug screening.
 XX
 SQ Sequence 314 AA;

Query Match 100.0%; Score 1564; DB 20; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2.4e-144;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRLLCWAALCLLGGADHTGAGVSTPSNKKVTEKGDVELRCDPISGHTALYWRSLGQ 60
 DB 1 mgrllcwaalcllgsdhtgagvstpsnkvtekgdvelrcdpisghtalywyrslgq 60
 QY 61 GPFEFLYFQGTGADSGPLNDRFFAVRPEGSVSTIKIQRTQEGDSAAYLKAGVAAAGWS 120
 DB 61 gpefllyfqtgagadsgplndrfavrpelsgsvstikiqrtedgdsaaylragvaagws 120
 QY 121 YNRYQYGPGRNLVLEDLKNVPEVAVPEPSAEISHTOKATVCLATGCFYDPDHVELSW 180
 DB 121 yneqyfgpgrnlvleldknvppevavpelpsaeishtokatlvcclatgcfydpdhvelsw 180
 QY 181 WVRGKEVHSGVSTDPQLKEQPALNDRSRYCLSLRLVSATFWQNPNRHRCQVQFYGLSE 240
 DB 181 wvrgekeshvsgvstdpqlkeqpaldnsryclslrlvsatfwqnpnrhrcqvqfyglse 240
 QY 241 NDEWTDQRAKPVTOIVSAEAWGADCGFTSESQQOQVLSATILYELLGKATLYAVLVSA 300
 DB 241 ndewtdqrapvtqvtsaeawgadcgftsyesqqoqvlsatillyellgkatlyavlvsa 300
 QY 301 LVLMAWVKRDSRG 314
 DB 301 lvlmawvkrkdsrg 314

RESULT 2

ID Y15229 standard; protein; 314 AA.

AC Y15229;

XX 26-OCT-1999 (first entry)

DE Human receptor protein (HURP); 8 amino acid sequence.

XX receptor; cancer; autoimmune disorder; inflammation;

KW antagonist; cell surface protein; cell signalling;

KW antibody; human receptor protein; HURP; reproductive disorder;

KW developmental disorder; gastrointestinal disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 205

FT /note= "Potential N-glycosylation site"

FT Misc-difference 312 /note= "Potential cAMP-/cGMP-dependent protein-
 FT kinase phosphorylation site"
 FT Misc-difference 101 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 133 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 152 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 239 /note= "Potential casein kinase II-
 FT phosphorylation site"
 FT Misc-difference 26 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 81 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 95 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 159 /note= "Potential protein kinase C-
 FT phosphorylation site"
 FT Misc-difference 212 /note= "Potential protein kinase C-
 FT phosphorylation site"
 XX WO9941375-A2.
 XX 19-AUG-1999.
 XX 05-FEB-1999; 99WO-US02572.
 XX 12-FEB-1998; 98US-0022939.
 XX (INCY-) INCYTE PHARM INC.
 XX Au-Young J, Bandman O, Baughn M, Corley NC, Guegler KJ;
 XX Hillman JL, Lal P, Shah P, Tang YT, Yue H;
 XX WPT: 1999-494536/41.
 XX N-FSDB: 206373.
 XX New human receptor proteins, used e.g. to treat, prevent and
 XX diagnose gastrointestinal and developmental disorders - and related
 XX nucleic acids, vectors, transformed cells, antibodies, agonists and
 XX antagonists
 PS Claim 1; Page 85-86; 94pp; English.
 XX The Human receptor protein 8 (HURP-8) shares 87% identity with
 CC human T-cell receptor beta.
 CC HURP-8 is expressed in cancerous, inflamed, haematopoietic/immune
 CC and gastrointestinal tissue. HURP-4 therefore appears to have a role in
 CC some forms of cancer, inflamed, haematopoietic/immune and
 CC gastrointestinal disorders.
 CC This gives rise to the possibility of using an antagonist or an antibody
 CC of HURP to treat or prevent cancer or autoimmune/inflammatory disorders.
 XX
 SQ Sequence 314 AA;

Query Match 85.18; Score 1433; DB 20; Length 314;

Best Local Similarity 86.6%; Pred. No. 3.1e-123;

Matches 272; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

QY 1 MGRLLCWAALCLLGGADHTGAGVSTPSNKKVTEKGDVELRCDPISGHTALYWRSLGQ 60

DB 1 mgrllcwwvflgtdhtgagvsgprykvakrgqdvrlcdpishghvsifwvqqalqg 60

QY	61	GPEFLYFGTGAADSGLPNDRFFAVPEGSVSTLKIQTQEGDSNAVILRAGVACWS	120
Db	61	gpelflyfneaqldksglpdrffaerpegsbstlkigrtdqdsavylcass:spagv	120
QY	121	YNEQYFGPGTRITVLIEDLKNVFPPEVAFPESEAEISHTQKATLVLCIATGFPDHFVLSW	180
Db	121	vdtyqfpgptritvledlknvfppeavafpeaeishtkqatlvclatgfpdhwelw	180
QY	181	WVNGKEVHSGVSTDFQPLKEQPALNDSRYCLSSRLRVSATFWONPRNHRFCQVFGYGLSE	240
Db	181	wvngkevhsgvatdbqpakegalndrsrlyclssrlrvsatfwnprnhrcqvfyglse	240
QY	241	NDEWTODRAKPVITQVSAEAWGRADCGFTSSYQGVLSATILYELLGKATLIYAVLVA	300
Db	241	ndewtdgrakpvtqivsaawgradcgftsesyqgvlstatiliyellgkatliyavlsa	300
QY	301	LVLMMVVRKRDGRG	314
Db	301	lvlmvmvvrkrdgrg	314
RESULT	3		
Y32208			
ID	Y32208	standard; Protein: 318 AA.	
XX	AC	Y32208;	
XX	AC	Y32208;	
XX	DT	15-FEB-2000 (first entry)	
XX	DE	Human receptor molecule (REC) encoded by Incyte clone 3428945.	
XX	KW	Receptor; REC: human; diagnosis: therapy; neoplastic disorder;	
XX	KW	immunological disorder; reproductive disorder; nervous disorder;	
XX	KW	gastrointestinal disorder; smooth muscle disorder;	
XX	KW	musculoskeletal disorder.	
XX	OS	Homo sapiens.	
XX	OS	WO99572720-A2.	
XX	PN	11-NOV-1999.	
XX	PD	28-APR-1999; 99WO-US09191.	
XX	PF	01-MAY-1998; 98US-0071822.	
XX	PR	(INCY-) INCYTE PHARM INC.	
XX	PA	Hillman JL, Bandman O, Tang YT, Yue H, Lal P, Corley NC;	
XX	PI	Guegler KJ, Patterson C;	
XX	PP	WPI; 2000-052971/04.	
XX	DR	N-PSDB; 234617.	
XX	DR		
XX	PT	Novel human receptor molecules used in the diagnosis, treatment and	
XX	PT	prevention of neoplastic, immunological, reproductive gastrointestinal,	
XX	PT	nervous, smooth muscle and musculoskeletal disorders	
XX	PS	Claim 1; Page 80-81; 94pp; English.	
XX	PS		
XX	CC	The present sequence represents a human receptor molecule (REC)	
XX	CC	encoded by Incyte cDNA clone 3428945. The invention provides human	
XX	CC	RECs and polynucleotides which identify and encode REC, as well as	
XX	CC	vectors, host cells, antibodies, agonists and antagonists. Human	
XX	CC	RECs appear to play a role in neoplastic, immunological,	
XX	CC	reproductive gastrointestinal, nervous, smooth muscle and	
XX	CC	musculoskeletal disorders. The protein, antagonists and agonists,	
XX	CC	and compositions can be used to treat: a reproductive disorder,	
XX	CC	including but not limited to, prolactin production disorders,	
XX	CC	infertility including tubal disease, ovulatory defects, endometriosis,	
XX	CC	disruptions of the estrous and menstrual cycles, polycystic ovary	
XX	CC	syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian	

RESULT 4
 Y69988
 ID Y69988 standard; Protein; 312 AA.
 AC Y69988;
 XX
 DT 31-MAY-2000 (first entry)
 XX
 DE Human receptor-associated protein from Incyte clone 2907954.
 XX
 KW Human receptor-associated protein; HRAP; Incyte clone 2907954;
 KW cytosolic; immunomodulatory; antiinflammatory; cardiant; antianaemic;
 KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
 KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
 KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
 KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
 KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
 KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
 KW multiple sclerosis; irritable bowel syndrome.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FT Modified-site 26
 FT /note= "Potential phosphorylation site"
 FT Modified-site 37
 FT /note= "Potential phosphorylation site"
 FT Modified-site 95
 FT /note= "Potential phosphorylation site"
 FT Modified-site 114
 FT /note= "Potential phosphorylation site"
 FT Modified-site 131
 FT /note= "Potential phosphorylation site"
 FT Modified-site 150
 FT /note= "Potential phosphorylation site"
 FT Modified-site 157
 FT /note= "Potential phosphorylation site"
 FT Modified-site 210
 FT /note= "Potential phosphorylation site"
 FT Modified-site 237
 FT /note= "Potential phosphorylation site"
 FT Modified-site 310
 FT /note= "Potential phosphorylation site"
 FT Modified-site 109
 FT /note= "Potential phosphorylation site"
 FT Modified-site 203
 FT /note= "Potential N-glycosylation site"
 FT
 FT
 WO200008155-A2.
 XX
 PD 17-FEB-2000.
 XX
 PF 06-AUG-1999; 99MO-US17777.
 XX
 PR 07-AUG-1998; 98US-0160065.
 PR 01-SEP-1998; 98US-0098703.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 XX Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
 PI Corley NC, Baughn MR;
 XX
 XX WPI: 2000-205710/18.
 DR N-PSDB: 250890.
 XX
 XX New human receptor-associated proteins (HRAP) useful for the diagnosis,
 PT treatment and prevention of cell proliferative, autoimmune,
 PT inflammatory, reproductive, cardiovascular, and gastrointestinal
 PT disorders
 XX
 PS Claim 1: Page 75; 99pp; English.
 XX

CC The present sequence is a human receptor-associated protein
 CC (HRAP) from Incyte clone 2907954 obtained from THYMOT05 cDNA library.
 CC This sequence is expressed in haematopoietic/immune, gastrointestinal
 CC and reproductive tissues. HRAP has cytostatic, immunomodulatory,
 CC antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic,
 CC antiasthmatic, antirheumatic, osteopathic, antiallergic, antianaemic,
 CC neuroprotective, diagnosis, treatment, prevention, reproductive disorder;
 CC cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
 CC gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
 CC arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
 CC multiple sclerosis; irritable bowel syndrome).
 XX
 SQ Sequence 312 AA;
 Query Match 81.2%; Score 1351; DB 21; Length 312;
 Best Local Similarity 83.0%; Pred. NO. 9.8e-116;
 Matches 264; Conservative 12; Mismatches 32; Indels 10; Gaps 2;
 QY 1 MCTRLCWAALCLIGADHTGAGVSOTPSNKYTEKGVLELRCDPISGHTALYWRQSLGQ 60
 DB 1 MCTRLCWAALCLIGADHTGAGVSOTPSNKYTEKGVLELRCDPISGHTALYWRQSLGQ 60
 QY 61 GPEFLTYFGTGAADSGLPNDRFFAVRPEGSVSTLKIQRTQDGSAAAYLRAGVAGWSS 120
 DB 61 GPKLLIQNGVVDSDQLPKDFSAERLKGVDSTLKIQPAKLEDSAVYLCA-----SS 114
 QY 121 Y----NEQYFGPGCTRLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPRV 176
 DB 115 FLDRNEDFFGPGTRTLTVLEDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPRV 174
 QY 177 ELSWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRSATFWQPNRHFRCQGFY 236
 DB 175 ELSWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRSATFWQPNRHFRCQGFY 234
 QY 237 GLSENDEWTDQRAKPVTVQIVSAEAWGRADCGFTSSYQGVLSATILYEILLGRATLYAV 296
 DB 235 GLSENDEWTDQRAKPVTVQIVSAEAWGRADCGFTSSYQGVLSATILYEILLGRATLYAV 294
 QY 297 LVSALVLMAMVKRKDSRG 314
 DB 295 LVSALVLMAMVKRKDSRG 312

RESULT 5
 Y69986
 ID Y69986 standard; Protein; 345 AA.
 AC Y69986;
 XX
 DT 31-MAY-2000 (first entry)
 XX
 DE Human receptor-associated protein from Incyte clone 1877651.
 XX
 KW Human receptor-associated protein; HRAP; Incyte clone 1877651;
 KW cytosolic; immunomodulatory; antiinflammatory; cardiant; antianaemic;
 KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
 KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
 KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
 KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
 KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
 KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
 KW multiple sclerosis; irritable bowel syndrome.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FT Modified-site 32
 FT /note= "Potential phosphorylation site"
 FT Modified-site 164


```

Db 178 wvngkevhsgvstdpqplkeqpalndsryclsrllrvsatfwnprnhfrqvgfylse 237
QY 241 NDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQGVLSTATILYEILLGKATLYAVLVA 300
Db 238 ndewtdqdrakpvtqivsaawgradcgftseyyqgvisatillyeillgkatlyavilva 297
QY 301 LVLMMVMKRRKDSRG 314
Db 298 lvlmmvmkrkdsrg 311

RESULT 7
P50079
ID P50079 standard; protein: 312 AA.
XX
AC P50079;
XX
DT 19-MAR-1992 (first entry)
XX
DE T-cell antigen receptor protein.
XX
KW T-cell receptor; DNA probe; tumor marker; ss.
XX
PN EP149548-A.
XX
PD 24-JUL-1985.
XX
PF 14-JAN-1985; 85EP-0300243.
XX
PR 06-FEB-1984; 84US-0577526.
XX
PA (ONTA-) ONTARIO CANCER INST.
XX
PI Mak TW;
XX
DR WPI; 1985-179193/30.
DR N-PSDB; N50091.
XX
PT New nucleic acid encoding T-cell antigen receptor polypeptide -
PT useful for prepn.. of probes or antibodies for detection of
PT tumour cells and T-cells
XX
PS Disclosure; Fig 3; 15pp; English.
XX
CC This protein resembles human and mouse Ig light chain
CC molecules. This protein is encoded by clone YF35 and is
CC part of the antigen receptor mediating specialized T-
CC lymphocyte function. Antibodies may be directed against
CC this protein and used for detection of T-cell receptor
CC antigen so that unknown cells, e.g. a tumor cell, can be
CC identified as a T-cell or other cell.
XX
SQ Sequence 312 AA;

Query Match 74.8%; Score 1244; DB 6; Length 312;
Best Local Similarity 77.1%; Pred. No. 5.9e-106;
Matches 242; Conservative 21; Mismatches 45; Indels 6; Gaps 2;

QY 1 MSTRLLCWAALCLLGADHTGAGVSTPSNKNVTEKGDVLRCDPISGHTALYWRQSLGQ 60
Db 1 mdswfccvslcilvakhtdagvlsprhevtmgqevtlrckpishghnsifwyrqtmnr 60
QY 61 GPEFLIYFOGTGAADSGPLNDRFFAVRPEGSVSTLKIQTQEGDSAAAYLRAGVAAGWSS 120
Db 61 glleliynnnvpidsgmpedrfakmpnasfstlkiqseprdsavf---cassfst 117
QY 121 YNEQY---FGPQTRTLVLEDLKNVFPPEVAVFEPSEAEISHTQKATLYCLATGYPDHVE 177
Db 118 csanygytfgsgrtlrvvedlnkvfppeavfepseaeishtqkatlyclatgfpdhve 177
QY 178 LSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWONPRNHFRCQVQFYG 237

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Db 178 lswwvngkevhsgvstdpqplkeqpalndsryclsrllrvsatfwnprnhfrqvgfyg 237
QY 238 lSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQGVLSTATILYEILLGKATLYAVL 297
Db 238 lSENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQGVLSTATILYEILLGKATLYAVL 297
QY 298 VSALVLMAMVKRKD 311
Db 298 vsalvlmamvkrkd 311

RESULT 8
P60471
ID P60471 standard; protein: 312 AA.
XX
AC P60471;
XX
DT 13-JUN-1991 (first entry)
XX
DE Portion of a human T-cell antigen receptor protein.
XX
KW Cancer; tumour cell; T-cell receptor.
XX
OS Homo sapiens.
XX
PN CAL197480-A.
XX
PD 03-DEC-1985.
XX
PF 01-FEB-1984; 84CA-0446545.
XX
PR 01-FEB-1984; 84CA-0446545.
XX
PA (ONTA-) ONTARIO CANCER INST.
XX
PI Mak TW;
XX
DR WPI; 1986-007147/02.
DR N-PSDB; N60406.
XX
PT New pure nucleic acid with sequence encoding T-cell polypeptide -
PT is prepd. by recombinant DNA methods for use as probe when
PT labelled and for antibody prodn.
XX
PS Claim 4; Fig 3; 22pp; English.
XX
CC Receptor protein product has at least 60% homology with the clone YF
CC 35. The product resembles human and mouse Ig light chain molecules,
CC and may be labelled for use as a probe for the detection of the
CC T-cell receptor antigen, and identification of unknown (esp. tumour
CC cells) as T-cells.
XX
SQ Sequence 312 AA;

Query Match 74.8%; Score 1244; DB 7; Length 312;
Best Local Similarity 77.1%; Pred. No. 5.9e-106;
Matches 242; Conservative 21; Mismatches 45; Indels 6; Gaps 2;

QY 1 MSTRLLCWAALCLLGADHTGAGVSTPSNKNVTEKGDVLRCDPISGHTALYWRQSLGQ 60
Db 1 mdswfccvslcilvakhtdagvlsprhevtmgqevtlrckpishghnsifwyrqtmnr 60
QY 61 GPEFLIYFOGTGAADSGPLNDRFFAVRPEGSVSTLKIQTQEGDSAAAYLRAGVAAGWSS 120
Db 61 glleliynnnvpidsgmpedrfakmpnasfstlkiqseprdsavf---cassfst 117
QY 121 YNEQY---FGPQTRTLVLEDLKNVFPPEVAVFEPSEAEISHTQKATLYCLATGYPDHVE 177
Db 118 csanygytfgsgrtlrvvedlnkvfppeavfepseaeishtqkatlyclatgfpdhve 177
QY 178 LSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWONPRNHFRCQVQFYG 237

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Db 178 lswvngkeivsgvstbqpklkeqpalndsrlyclssrlrvsatfwnprnhfrcoqvfyg 237
QY 238 LSEDEWTDQRAKPYTQIVSAEAWGRADCGFTSESYOQGVLSATILYEILLGKATLYAVL 297
DB 238 lsewtdqdrakpvtqivsaeeawgradcgftsvsyqgvlsatillyeillgkatlyavl 297
QY 298 VSALVLMAMVKRKD 311
DB 298 vsalvlmamvkrkd 311

RESULT 9
R53145
ID R53145 standard; Protein; 312 AA.
XX AC R53145;
XX DT 08-SEP-1994 (first entry)
XX DE T-cell antigen receptor.
XX KW T-cell antigen receptor; T-lymphocyte; probe; hybridization; MOLT-3.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 90 /note= "possible N-glycosylation site"
FT Misc-difference 205 /note= "possible N-glycosylation site"
XX EP593092-A..
XX PD 20-APR-1994.
XX PF 14-JAN-1985; 85EP-0118695.
XX PR 13-JAN-1984; 84US-0570694.
XX PR 06-FEB-1984; 84US-0577526.
XX PA (ONTA-) ONTARIO CANCER INST.
XX PI Mak TW;
XX WPI; 1994-127936/16.
XX DR N-PSDB; Q62128.
XX New nucleic acid encoding T-cell antigen receptor - is useful
PT e.g. as a probe to identify T-cells
XX Disclosure; Fig 3; 13pp; English.
XX mRNA complementary to the DNA sequence given in Q62128 is obtained by
CC isolating mRNA from MOLT-3 cells, preparing cDNA, inserting the cDNA
CC into the BglII site of vector pFP502BB5, transfecting the vector into
CC Escherichia coli HB101, and screening for 1.3 kb T-cell specific
CC mRNA in MOLT-3 and HSC-58 cells. The mRNA encodes a portion of the
CC T-cell antigen receptor (sequence R53145).
XX Sequence 312 AA;
SQ

Query Match 73.9%; Score 1230; DB 15; Length 312;
Best Local Similarity 76.8%; Pred. NO. 1.1e-104;
Matches 241; Conservative 21; Mismatches 46; Indels 6; Gaps 2;

QY 1 MGRRLICWALCLLGADHDGAGVSQTPSNKYTEKGDKDELRCDPISCHTALYWRQLCQ 60
DB 1 mdswtfcvscilvakhdagdvigprhevtmgdevlrcpksghnslfsyrtqmmr 60
QY 61 GPEFLYFQCTGAADSGLPNDRFFAVRPEGSYSTLKIQRTQCGDGAAYLRAGVAAGWSS 120
DB 61 glallyfnnnvidsgmpedrfakmpnasfstlikipseprdsavf---cassfst 117

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QY 121 YNEQY---FGPGRLTVLEDLKNVFPPEVAFPESEAEISHTOKATLVCLATGYPDHVE 177
DB 118 csanygytfgsgtrltvvedlnkvfppeavafpseaeishtqkatlvclatgfpdhve 177
QY 178 LSWWNGKEVHSGVSTDPOLKEPALNDSRYLCLSSRLRVSATFWQNPNRHFRCOQVFG 237
DB 178 lswwngkevnsgvstbqpklkeqpalndsrlyclssrlrvsatfwnprnhfrcoqvfyg 237
QY 238 LSEDEWTDQRAKPYTQIVSAEAWGRADCGFTSESYOQGVLSATILYEILLGKATLYAVL 297
DB 238 lsewtdqdrakpvtqivsaeeawgradcgftsvsyqgvlsatillyeillgkatlyavl 297
QY 298 VSALVLMAMVKRKD 311
DB 298 vsalvlmamvkrkd 311

RESULT 10
Y69999
ID Y69999 standard; Protein; 316 AA.
XX AC Y69999;
XX DT 31-MAY-2000 (first entry)
XX DE Human receptor-associated protein from Incyte clone 2656082.
XX KW Human receptor-associated protein; HRAP; Incyte clone 2656082;
KW cytosolic; immunomodulatory; antiinflammatory; cardiant; antianemic;
KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW gastritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW multiple sclerosis; irritable bowel syndrome.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Protein 23..316 /label= Mature_HRAP
FT Domain 35..112 /label= Immunoglobulin-like_domain
FT Domain 161..235 /label= Immunoglobulin-like_domain
FT Domain 286..306 /label= Transmembrane_domain
FT Modified-site 26 /note= "Potential phosphorylation site"
FT Modified-site 35 /note= "Potential phosphorylation site"
FT Modified-site 39 /note= "Potential phosphorylation site"
FT Modified-site 57 /note= "Potential phosphorylation site"
FT Modified-site 69 /note= "Potential phosphorylation site"
FT Modified-site 135 /note= "Potential phosphorylation site"
FT Modified-site 154 /note= "Potential phosphorylation site"
FT Modified-site 161 /note= "Potential phosphorylation site"
FT Modified-site 214 /note= "Potential phosphorylation site"
FT Modified-site 241 /note= "Potential phosphorylation site"
FT Modified-site 314 /note= "Potential phosphorylation site"
FT Modified-site /note= "Potential phosphorylation site"

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FT Modified-site 76 /note= "N-glycosylation site"
 FT Modified-site 89 /note= "N-glycosylation site"
 FT Modified-site 207 /note= "N-glycosylation site"
 FT XX
 FT XX W0200008155-A2.
 FT XX
 FT XX 17-FEB-2000.
 FT XX
 FT XX 06-AUG-1999; 99WO-US17777.
 FT XX
 FT XX 07-AUG-1998; 98US-0160065.
 FT XX 01-SEP-1998; 98US-0098703.
 FT XX
 FT XX (INCY-) INCYTE PHARM INC.
 FT XX
 FT XX Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
 FT XX Corley NC, Baughn MR;
 FT XX
 FT XX WPI; 2000-205710/18.
 FT XX N-PSDB; 250901.
 FT XX
 FT XX New human receptor-associated proteins (HRAP) useful for the diagnosis,
 FT XX treatment and prevention of cell proliferative, autoimmune,
 FT XX inflammatory, reproductive, cardiovascular, and gastrointestinal
 FT XX disorders -
 FT XX
 FT XX Claim 1; Page 86; 99pp; English.
 FT XX
 FT XX The present sequence is a human receptor-associated protein
 FT XX (HRAP) from Incyte clone 2656082 obtained from THYMNOF04 cDNA library.
 FT XX This sequence is expressed in haematopoietic/immune, gastrointestinal
 FT XX and reproductive tissues. HRAP has cytostatic, immunomodulatory,
 FT XX antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic,
 FT XX antiarthritic, antirheumatic, osteopathic, antiallergic, antianaemic,
 FT XX antiasthmatic, antidiabetic, dermatological and neuroprotective
 FT XX activities. The present sequence is useful in the diagnosis, treatment
 FT XX and prevention of disorders associated with HRAP expression, especially
 FT XX cell proliferative, autoimmune/inflammatory, reproductive,
 FT XX cardiovascular and gastrointestinal disorders (e.g. atherosclerosis,
 FT XX cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia,
 FT XX asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and
 FT XX irritable bowel syndrome).
 FT XX
 FT XX Sequence 316 AA;

Query Match 71.0%; Score 1182; DB 21; Length 316;
 Best Local Similarity 74.1%; Pred. No. 2.8e-100;
 Matches 237; Conservative 18; Mismatches 55; Indels 10; Gaps 3;

QY 1 MGRLLCWAALCLLGGADHTGAGVSQTPSNKVKTEKGDVLRDPTSGHTALWYQSLSQ 60
 DB 1 mgrllccavllcllgavpmetgtqtrhlvmgntnkkalkceqhlghnamwykgsakk 60
 QY 61 GPFLIYFOGTGAADSGLPNDPFFAVRPEGSVSTLKIQRTQEGDSSAAVIRA-----GV 114
 DB 61 plelmfvysleervennsvps-rfpecpnsshlflhlhtlcpedsalylcaassqvhpgi 119
 QY 115 AAGWSYNSQYFGPGTRRLVLESDLNKVPPEVAVPEPSEAEISHTQKATFLVCLATGFGFPD 174
 DB 120 adg---lneqifpgptrltvlledlnkvfppevavfepseaeishtqkatlvcclatgfyd 176
 QY 175 HVLSWWNGKEVHSGVSTDPPLKEQPALNDSRYCLSLRVSATFWONPRNHFRCOVQ 234
 DB 177 hvlswwngkevnsgvstcdpplkqpalndsrlyclsrfrvsatfwnprnhfrcqvq 236
 QY 235 FYGLSENDEWTDQRAKPVQIYSAEAWGRADCGFTSESYQQQVLSATILYEILLGKATLY 294
 DB 237 fyglsendewtdqrakpvtqivsaawgradcgftsesyqgqvlstallyeillgkatly 296

QY 295 AVLSALVLMAMVKRKDSRG 314
 DB 297 avlsalvilmamvkrkdsrg 316
 RESULT 11
 Y51069
 ID Y51069 standard; protein; 179 AA.
 XX
 XX AC Y51069;
 XX
 XX 22-MAR-2000 (first entry)
 XX
 XX Human TCRbeta protein fragment #2.
 XX
 XX T cell receptor beta; TCRbeta; human; constant region;
 XX immunosuppressor.
 XX
 XX Homo sapiens.
 XX
 XX JP11302299-A.
 XX
 XX 02-NOV-1999.
 XX
 XX 21-APR-1998; 98JP-0110607.
 XX
 XX 21-APR-1998; 98JP-0110607.
 XX
 XX (KIRI) KIRIN BREWERY KK.
 XX
 XX WPI; 2000-075345/07.
 XX
 XX T cell receptor beta chain constant region peptide - has
 XX immunosuppressing activity
 XX
 XX Claim 4; Page 12-13; 15pp; Japanese.
 XX
 XX This invention describes a novel polypeptide comprising substantially
 XX part or all of the constant region of T cell receptor beta chain
 XX (TCRbeta) and containing substantially no other regions of TCRbeta and
 XX having immunosuppressing activity. The TCRbeta requires no consideration
 XX of tissue-compatible antigen for the patient to be dosed nor of antigen
 XX specificity. This sequence represents a fragment of the human TCRbeta
 XX protein described in the method of the invention.
 XX
 XX Sequence 179 AA;

Query Match 56.7%; Score 944; DB 21; Length 179;
 Best Local Similarity 100.0%; Pred. No. 7.5e-79;
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 EDLKNVPPEVAVPEPSEAEISHTQKATFLVCLATGFGFPDHFVLSWWNGKEVHSGVSTDP 195
 DB 1 edlknvppevavfepseaeishtqkatlvcclatgfydhlvlswwngkevhsgvstdp 60
 QY 196 QPLKEQPALNDSRYCLSLRVSATFWONPRNHFRCOVQFVGLSENDEWTDQRAKPVTOI 255
 DB 61 qplkeqpalndsrlyclsrfrvsatfwnprnhfrcqvfyglsendewtdqrakpvtqi 120
 QY 256 VSAEAWGRADCGFTSESYQQQVLSATILYEILLGKATLYAVLSALVLMAMVKRKDSRG 314
 DB 121 vsaeawgradcgftsesyqgqvlstallyeillgkatlyavlvsalvlmamvkrkdsrg 179
 RESULT 12
 Y05403
 ID Y05403 standard; Protein; 303 AA.
 XX
 XX AC Y05403;
 XX
 XX 02-JUL-1999 (first entry)
 XX

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DE   Killer T-cell receptor protein sequence.
XX
KW   Killer T-cell receptor; HIV; infection; HIV-1 IIIB; therapy.
OS   Mus musculus.
XX   WO9916885-A1.
PN   PD
XX   08-APR-1999.
XX   28-SEP-1998; 98WO-JP04345.
XX   26-SEP-1997; 97JP-0262536.
XX   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAIT/) SAITO T.
PA   (TAKA/) TAKAHASHI H.
XX   Saito T, Takahashi H;
PI
XX   WPI: 1999-255096/21.
DR   N-PSDB; X36391.
XX
XX   Killer T-cell receptor peptide specifically recognizing HIV-infected
PT   cells
XX
PS   Claim 7; Page 60-62; 75pp; Japanese.
XX
XX   This sequence is a killer T-cell receptor protein of the invention,
CC   which recognises and damages cells infected with human immunodeficiency
CC   virus (HIV), especially with HIV-1 IIIB. The receptor can be used as
CC   a constituent of compositions for the treatment of HIV infection.
XX
SQ   Sequence 303 AA;

Query Match      55.6%; Score 925.5; DB 20; Length 303;
Best Local Similarity 60.3%; Pred. No. 7.6e-77;
Matches 188; Conservative 34; Mismatches 81; Indels 9; Gaps 4;

QY   1 MTRILLWALCLLGADHFGAGVSTPNKVTKEGKDVLCRDPYSGHTALYWRQSLGQ 60
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   1 mgsrif-fvllllcalkhmeaavtgsrskvavtggkvltlchgtnndymwyrgdgh 59
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   61 GPEFLIFYFGTGAADSLPNDREFFAVRPEGSVSTLKIQTREQGDSAAVLRAGVAAGWSS 120
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   60 glrlhysvvaadstekgdip-dgykasrpsqenfsllleaslsqavf---cassegr 115
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   121 YNEQYFGPGTRITLVLEDLKNVPEPPEVAVPEPSEAEISHTQKATLVCLATGFPYDPDHVELSW 180
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   116 eaefgfgpqrtrltvledlrnvtppkvsllfepskaeiankqkatlvclargffpdhvelsw 175
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   181 WYNGKEVHSGVSTDRQPLKEQPALNDSRYCLSSRLRVSATFWQNPNNHFRQVQFYGLSE 240
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   176 wvngkevhsgvstdrpqayke---snysylssrllrvsatfwqnpnnhfrqvgfhgise 231
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   241 NDEWTQDRAKPTQIVSAPAWGRACGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   232 edkwpegsqkptqnisaeaawgradcgttsasyhgvisatilyeillgkatlyavlvsg 291
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   301 LVLMMAMVKRKDS 312
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   292 lvlmamvkkkns 303
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 13
Y51068
ID   Y51068 standard; protein; 177 AA.
XX
AC   Y51068;
XX
DT   22-MAR-2000 (first entry)
XX

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DE   Human TCRbeta protein fragment #1.
XX
KW   T cell receptor beta; TCRbeta; human; constant region;
XX   immunosuppressor.
OS   Homo sapiens.
XX   JP11302299-A.
PN   PN
XX   02-NOV-1999.
XX   21-APR-1998; 98JP-0110607.
XX   21-APR-1998; 98JP-0110607.
XX   (KIRI ) KIRIN BREWERY KK.
PA   PA
XX   WPI: 2000-075345/07.
DR   DR
XX   T cell receptor beta chain constant region peptide - has
PT   immunosuppressing activity
XX
PS   Disclosure; Page 11; 15pp; Japanese.
XX
XX   This invention describes a novel polypeptide comprising substantially
CC   part or all of the constant region of T cell receptor beta chain
CC   (TCRbeta) and containing substantially no other regions of TCRbeta and
CC   having immunosuppressing activity. The TCRbeta requires no consideration
CC   of tissue-compatible antigen for the patient to be dosed nor of antigen
CC   specificity. This sequence represents a fragment of the human TCRbeta
CC   protein described in the method of the invention.
XX
SQ   Sequence 177 AA;

Query Match      54.5%; Score 907; DB 21; Length 177;
Best Local Similarity 97.7%; Pred. No. 1.8e-75;
Matches 172; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY   136 EDLKNVPEPPEVAVPEPSEAEISHTQKATLVCLATGFPYDPDHVELSWVNGKEVHSGVSTDP 195
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   1 edlnkvfppevavfepseaeishtqkatlvclatgffpdhvelswvngkevhsgvstdp 60
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   196 QPLKEQPALNDSRYCLSSRLRVSATFWQNPNNHFRQVQFYGLSENDEWTQDRAKPTQI 255
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   61 qplkeqpaldndsrlyclssrlrvsatfwqnpnnhfrqvgfyglisendewtqdrakptqi 120
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY   256 VSAEAWGRACGFTSESYQQGVLSATILYEILLGKATLYAVLVSAALVLMAMVKRKD 311
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB   121 vsaeawgradcgttsyqgvlsatilyeillgkatlyavlvlsalvlmamvkrkd 176
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 14
P50252
ID   P50252 standard; Protein; 306 AA.
XX
AC   P50252;
XX
DT   07-OCT-1991 (first entry)
XX
DE   Sequence of T-cell antigen receptor beta chain encoded by cDNA
DE   clone 86T1.
XX
XX   Diagnosis; site-directed therapy.
XX
OS   Homo sapiens.
XX
XX   Key      Location/Qualifiers
FT   Peptide 1..19
FT           /label= leader
FT   Region 20..117
FT           /label= variable
FT   Region 118..133

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 11, 2000, 06:08:11 ; Search time 12.56 Seconds
(without alignments)
419.030 Million cell updates/sec

Title: US-09-405-940-1
Perfect score: 1664
Sequence: 1 MGRRLCWAALCLLGADHTG.....AVLSALVLMVMVKRDSRG 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCBUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1664	100.0	314	3	US-08-897-097-1
2	1394.5	83.8	311	3	US-08-897-097-3
3	1332	80.0	310	3	US-08-897-097-4
4	895	53.8	314	5	5434340-7
5	868.5	52.2	293	5	5189147-3
6	827	49.7	391	4	PCT-US95-15696-2
7	707	42.5	266	5	5175384-11
8	584.5	35.1	217	5	5189147-7
9	265	15.9	102	3	US-08-466-368-9
10	243.5	14.6	236	3	US-08-487-580-10
11	239	14.4	234	3	US-08-487-550-2
12	237	14.2	235	2	US-08-378-939-12
13	236.5	14.2	215	2	US-08-480-753-8
14	228.5	13.7	213	3	US-08-630-820-6
15	224	13.5	241	2	US-07-916-098A-56
16	222.5	13.4	232	1	US-08-704-744-80
17	222.5	13.4	239	3	US-08-487-550-6
18	220.5	13.3	214	1	US-08-458-516-12
19	220.5	13.3	274	1	US-08-256-964A-19
20	219	13.2	242	1	US-08-398-613A-56
21	219	13.2	242	1	US-08-398-612A-56
22	219	13.2	242	1	US-08-398-611A-56
23	219	13.2	242	2	US-08-491-334A-56
24	219	13.2	242	3	US-09-027-449-42
25	219	13.2	242	3	US-08-804-444A-42
26	216.5	13.0	218	2	US-08-887-352B-15
27	216.5	13.0	218	2	US-08-887-352B-17
28	216.5	13.0	218	2	US-08-887-352B-19

29 216.5 13.0 218 2 US-08-887-352B-24
30 213.5 12.8 237 1 US-08-398-612A-28
31 213.5 12.8 237 1 US-08-398-611A-28
32 213.5 12.8 237 2 US-08-491-334A-28
33 213.5 12.8 237 3 US-09-027-449-25
34 213.5 12.8 237 3 US-08-804-444A-25
35 213.5 12.8 238 1 US-08-398-613A-28
36 213 12.8 233 2 US-07-934-373C-25
37 213 12.8 233 3 US-08-437-642B-25
38 213 12.8 233 4 PCT-US93-07832-25
39 212.5 12.8 219 1 US-08-353-400-34
40 212.5 12.8 237 2 US-08-463-587A-25
41 212.5 12.8 237 2 US-08-463-667A-3
42 212.5 12.8 237 3 US-08-923-854-25
43 212.5 12.8 237 4 PCT-US91-09133-26
44 212.5 12.8 239 1 US-08-353-400-37
45 212 12.7 214 2 US-08-480-753-6

ALIGNMENTS

RESULT 1
US-08-897-097-1
; Sequence 1, Application US/08897097
; Patent No. 6054292
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,097
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0346 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TONGTUT01
; CLONE: 983910
US-08-897-097-1

Query Match 100.0%; Score 1664; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 Db 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 QY 61 GPEFLIYFQGTGAADSGLPNDREFFAVRPEGSVSTLKIQRTQEGDAAALYLRAGVAAAGWS 120
 Db 61 GPEFLIYFQGTGAADSGLPNDREFFAVRPEGSVSTLKIQRTQEGDAAALYLRAGVAAAGWS 120
 QY 121 YNEQYFGPCTRLTVLEDLKNNVFPPEVAVPEPSEAEISHTQKATLYCLATGFPDHPVLSW 180
 Db 121 YNEQYFGPCTRLTVLEDLKNNVFPPEVAVPEPSEAEISHTQKATLYCLATGFPDHPVLSW 180
 QY 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQPNRHFRCQVQFGLSE 240
 Db 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQPNRHFRCQVQFGLSE 240
 QY 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
 Db 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
 QY 301 LVLMMVKRKDSRG 314
 Db 301 LVLMMVKRKDSRG 314

RESULT 2

US-08-897-097-3
 ; Sequence 3, Application US/08897097
 ; Patent No. 6054292
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,097
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0346 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 311 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1100182
 ; US-08-897-097-3

Query Match 83.8%; Score 1394.5; DB 3; Length 311;
 Best Local Similarity 85.4%; Pred. No. 6.3e-141;
 Matches 268; Conservative 14; Mismatches 29; Indels 3; Caps 2;
 QY 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 Db 1 MSTRLLCWAALCLLGGADHTGAGYSQTPSNKVTETKGDVELRCDPISGHTALYWRQSLGQ 60
 QY 61 GPEFLIYFQGTGAADSGLPNDREFFAVRPEGSVSTLKIQRTQEGDAAALYLRAGVAAAGWS 120
 Db 61 GPEFLIYFQGTGAADSGLPNDREFFAVRPEGSVSTLKIQRTQEGDAAALYLRAGVAAAGWS 120
 QY 121 YNEQYFGPCTRLTVLEDLKNNVFPPEVAVPEPSEAEISHTQKATLYCLATGFPDHPVLSW 180
 Db 121 YNEQYFGPCTRLTVLEDLKNNVFPPEVAVPEPSEAEISHTQKATLYCLATGFPDHPVLSW 180
 QY 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQPNRHFRCQVQFGLSE 240
 Db 181 WNGKEVHSGVSTDPQPLKEQPALNDSRYCLSRRLVSATFWQPNRHFRCQVQFGLSE 240
 QY 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
 Db 241 NDEWTDRAKPVTVQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKATLYAVLVSA 300
 QY 301 LVLMMVKRKDSRG 314
 Db 301 LVLMMVKRKDSRG 314

RESULT 3

US-08-897-097-4
 ; Sequence 4, Application US/08897097
 ; Patent No. 6054292
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,097
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0346 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 310 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:

LIBRARY: GenBank
CLONE: 339012
US-08-897-097-4

Query Match 80.0%; Score 1332; DB 3; Length 310;
Best Local Similarity 81.7%; Pred. No. 3e-134;
Matches 254; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

QY 1 MGRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQ 60
DB 1 MGRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQ 60

QY 61 GPEFLYFQGTGAADSLNDPFAVRPEGSVSTLKIQRTQEGDSAAYLRAVGAAGWSS 120
DB 61 GPEFLYFQGTGAADSLNDPFAVRPEGSVSTLKIQRTQEGDSAAYLRAVGAAGWSS 120

QY 121 YNEQYFGPTRLVLEDLKNVPPEVAVPEPSEAEISHTQKATLVCLATGYPDHVELSW 180
DB 120 -QPHFGDGTRLSLEDLKNVPPEVAVPEPSEAEISHTQKATLVCLATGYPDHVELSW 178

QY 181 WVGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRQVQFYGLSE 240
DB 179 WVGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRQVQFYGLSE 238

QY 241 NDEWTDRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVA 300
DB 239 NDEWTDRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVA 298

QY 301 LVLMAVKKRD 311
DB 299 LVLMAVKKRD 309

RESULT 4
5434340-7
Patent No. 5434340
APPLICANT: KRIMPENFORD, PAULUS J.A.; BERNS, ANTONIUS J.M.
TITLE OF INVENTION: TRANSGENIC MICE DEPLETED IN MATURE
T-CELLS AND METHODS FOR MAKING TRANSGENIC MICE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
FILING DATE: 27-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 280,218
FILING DATE: 05-DEC-1988
SEQ ID NO: 7
LENGTH: 314
5434340-7

Query Match 53.8%; Score 895; DB 5; Length 314;
Best Local Similarity 58.7%; Pred. No. 1.5e-87;
Matches 182; Conservative 34; Mismatches 86; Indels 8; Gaps 3;

QY 3 TRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGP 62
DB 13 TRLLCWAALCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGP 62

QY 63 EFLYFQGTGAADSLNDPFAVRPEGSVSTLKIQRTQEGDSAAYLRAVGAAGWSSYN 122
DB 73 RLHYSGVSTXQFAVKE----SNYSYCLSSRLRVSAFWQNPNNHFRQVQFYGLSE 128

QY 123 EQYFGPTRLVLEDLKNVPPEVAVPEPSEAEISHTQKATLVCLATGYPDHVELSWV 182
DB 129 TLFGSGTRTLVLEDLKNVPPEVAVPEPSEAEISHTQKATLVCLARGFPDHHVELSWV 188

QY 183 NGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRQVQFYGLSE 242
DB 189 NGKEVHSGVSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRQVQFYGLSE 244

QY 243 EWTQDRAKPTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVA 302

DB 245 KWPEGSPKPVTONISAEAWGRADCGITSASYHQGVLSATILYELLGKATLYAVLVA 304
QY 303 LMAVKKRDS 312
DB 305 LMAVKKRNS 314

RESULT 5
5189147-3
Patent No. 5189147
APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSSEN, HERMAN N.;
TONEGAWA, SUSUMU
TITLE OF INVENTION: METEROIDIMERIC T LYMPHOCYTE RECEPTOR
ANTIBODY
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/271,216
FILING DATE: 14-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 666,988
FILING DATE: 31-OCT-1984
APPLICATION NUMBER: 620,122
FILING DATE: 13-JUN-1984
SEQ ID NO: 3
LENGTH: 293
5189147-3

Query Match 52.2%; Score 868.5; DB 5; Length 293;
Best Local Similarity 57.9%; Pred. No. 9.4e-85;
Matches 175; Conservative 34; Mismatches 82; Indels 11; Gaps 3;

QY 11 LCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGPFLYFQ 70
DB 3 LCLLGADHTGAGVSQTPSNKVKTEKGDVLRCDPISGHTALYRWYRSLGQGPFLYFQ 62

QY 71 TGAADSLNDPFAVRPEGSVSTLKIQRTQEGDSAAYLRAVGAAGWSSYNEQYFGGT 130
DB 63 VDSNSEGDPKG-YRVSRKKREHFLSLDLSAKTNTSYVFCAGAP-----EQYFGGT 115

QY 131 RLTVLEDLKNVPPEVAVPEPSEAEISHTQKATLVCLATGYPDHVELSWVNGKEVHSG 190
DB 116 RLTVLEDLKNVPPEVAVPEPSEAEISHTQKATLVCLARGFPDHHVELSWVNGKEVHSG 175

QY 191 VSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRQVQFYGLSENDEWTDRAK 250
DB 176 VSTDPOPLKEDPALNDSRYCLSSRLRVSAFWQNPNNHFRQVQFYGLSENDEWTDRAK 231

QY 251 PVTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVA 310
DB 232 PVTQIVSAEAWGRADCGFTSESYQQGVLSATILYELLGKATLYAVLVA 291

QY 311 DS 312
DB 292 NS 293

RESULT 6
PCR-US95-15696-2
Sequence 2, Application PC/TUS9515696
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College
TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: Maine
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:


```
/
/ TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
/ TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper & Dunham LLP
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,368
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 24577-E1-B/JPW/AKC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0525
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 102 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ANTI-SENSE: YES
/ FEATURE:
/ NAME/KEY: Active-site
/ LOCATION: 1..102
/
/ US-08-466-368-9
/
/ Query Match 15.9%; Score 265; DB 3; Length 102;
/ Best Local Similarity 56.5%; Pred. No. 5.5e-21;
/ Matches 52; Conservative 12; Mismatches 28; Indels 0; Gaps 0;
/
/ QY 21 AGVSTPSNKVTEKGKDVLRCDPISGHTALVWYRSLGCGPEFLIYFGGTGAADSGLP 80
/   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
/ Db 2 AGVIQSPRHEVTGQEVTLRCKPISGHSLEWYRQTMKGLLELLIYFNNNVPIDDSGMP 61
/
/ QY 81 NDRFFAVRPEGSVTLKIQRTEQGSAAVYLA 112
/   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
/ Db 62 EDFSAKMPNASFTLKIQSPRDSAVYFCA 93
/
/ RESULT 10
/ US-08-487-550-10
/ Sequence 10, Application US/08487550
/ Patent No. 6113898
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Darrell R.
/ TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
/ TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
/ AND USE THEREOF AS
/ IMMUNOSUPPRESSANTS"
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22314
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,368
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: teskin, Robin L.
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 012712-131
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-836-6620
/ TELEFAX: 703-836-2021
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 236 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-487-550-10
/
/ Query Match 14.6%; Score 243.5; DB 3; Length 236;
/ Best Local Similarity 34.4%; Pred. No. 4.1e-18;
/ Matches 77; Conservative 31; Mismatches 77; Indels 39; Gaps 12;
/
/ QY 23 VSQTPSNKVTEKGKDVLRCDPISGHTA-----LYWYRSLGCGPEFLIYFGGTGAADD 76
/   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
/ Db 30 VSGAPGQKVT-----TGSTNIGGYDLHWYQQLPGTAPKLLIY-----DI 72
/
/ QY 77 SGLP---NDRFFAVRPEGSVTLKIQRTEQGSAAVYLAAGVWSSYNEQYFGPGTGLT 133
/   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
/ Db 73 NKRPSGISDRFSGSK-SGTAASLAITGLQTEDEADYQSYD---SSLNAQVFGGTGLT 128
/
/ QY 134 VLEDLKNVFPPEVAVPEPSEABISHTQKATLVCLATGYPDPHVELSWWYNGKEVHSGVST 193
/   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
/ Db 129 VLGQPKAA--PSVTLPFPSSSEL-QANKATLVCLISDFYPGAIVTAMKADSSPVKAGVET 185
/
/ QY 194 DPQPLKEQPALNDSRYCLSLRLVSATFQWQPNRHFRCQVQFYG 237
/   | : : : | | | | | | | | | | | | | | | | | | | | | | | | |
/ Db 186 -TTPSKQ---SNKYAASSYLSLTPQWKSQRS-YSCQVTHEG 223
/
/ RESULT 11
/ US-08-487-550-2
/ Sequence 2, Application US/08487550
/ Patent No. 6113898
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Darrell R.
/ TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
/ TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
/ AND USE THEREOF AS
/ IMMUNOSUPPRESSANTS"
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
/ STREET: 699 Prince Street
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22314
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,550
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
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